

FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTTCAGATCTGCTCGGTAGA
 CCTGGTGCACCACCACCA**ATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
 GTTTTCCACCAGCTTTTCACCAAGGCCTCCCCTGTTGTGAAGAATTCCATCAGGAAGATCA
 ATGGCTGTTAACACCTAGCAGGGAATATGCCACCAAAACAAGAATTGGGATCCGGCGTGGGA
 GAAGTGGCCCAAGAACTCAAAGAGGCAGCATTTGGAAACCATCGATGGAAAAATATTTAAATTT
 GATCAGATGGGAAGATGGTTTGTGTGCTGGAGGGGCTGCTGTTGGTCTTTGGAGCATTTGTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCCTCAGT
 ATGTCAAGGATAGAATTCATTCCACCTATATGTACTTAGCAGGGAGTATTGGTTAACAGCT
 TTGTCGCCATAGCAATCAGCAGAACGCCCTGTTCTCATGAACCTTCATGATGAGAGGCTCTTG
 GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCCAGGCCAAAGCATCTGCTGGTTGCTACATTCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCTCTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTTGGGAGGCCCTCTCCACTGTGGCCATGTGTGCGCCACAGTGAAAAGTTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCCCTGGGTCTCGTCTTTGTGTCCTCATTGGGATCTATG
 TTTCTTCCACCTACCACCGTGGCTGGTGCCACTCTTTACTCAGTGGCAATGTACGGTGGATT
 AGTTCCTTTTCAGCATGTTCTCTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT
 CACCAATGTATGGAGTTCAAAAAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
 ACATTAATATATATTTATCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAAAT**G**
AAGTGACTCAGCTTCTGGCTTCTCTGCTACATCAATATCTTGTTTAATGGGGCAGATATGC
 ATTAATAGTTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTCATCATA
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTTTTTCTGGAGAATAAATGCAGT
 AATCCTCTCCCAATAAGCACACACATTTCAATTCTCATGTTTGAAGTATTTTAAATGTT
 TTGGTGAATGTGAAAACATAAGTTTGTGTCTGAGAATGTAAGTCTTTTTCTACTTTAAAA
 TTTAGTAGGTTCACTGAGTAACATAAAATTTAGCAAACTGTGTTGTCATATTTTTTTGGAGT
 GCAGAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGGACAGAGAGAAG
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTTGTTATTGATTA
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTGGAACCAAGTGGTCATTGTTACATTCATTT
 GCTGAACTTAACAAAACCTGTTATCCTGAAACAGGCACAGGTGATGCAATTCCTGCTGTTG
 CTTCTCAGTGCTCTCTTTCCAATATAGATGTGGTCATGTTTGAAGTTGACAGAATGTTAATC
 ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTACTTTTGAATGTTACAAAAGGAA
 ATAACCTTTAAACATATTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTGCTTTTCCAG
 AATACAAACAGTATACATCATG

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWFVAGGAAVGLGALCYYGGLSNEIGAIEKAVIWPQYVKDRI
HSTMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTFAAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTLGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLV FVSSSLGSMFLPPTTVAGATLYSVAMYGGVLVFSMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCCGCCCCGTCTCCGCCTTCTGCAT
 CGCGGCTTCGGCGGCTTCACCTAGACACCTAACAGTCCGGGAGCGCGGCCGCTCGTAGGG
 GGTCCGGACGGGGAGTCCGGCGGTCTTGGTCATCTTGGCTACCTGTGGGTCCGAAG**ATGT**CGG
 ACATCGGAGACTGGTTTCAGGAGCATCCCGGCGATCAGCGCTATTGGTTCCGCCGCCACCGTC
 GCGGTGCCCTTGGTCCGCAAACTCGGCGCTCATCGCCCGGCTACCTCTTCCCTCTGGCCCGA
 AGCCTTCCCTTATCGCTTTCAGATTTGGAGGCCAATCACTGCCACCTTATTTCCCTGTGGT
 TCCAGGAACCTGGATTTCTTTTATTTGGTCAATTTATATTCTTATATCATGATTTCTACGCGG
 CTTGAAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTATTATCATGCTCCCTCTTAACTG
 GATTTGCATCGTGATTACTGGCTTAGCAATGGATATCGAGTTGCTGATGATTCCTCTGATCA
 TGTGACTACTTTATGTCTGGGCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTTGGGA
 ACACGATTTAAGGCCGTGCTATTTACCTGGGTATCCTTGGATTCAACTATATCATCGGAGG
 CTCGGTAAATCAATGAGCTTATTGGAATCTGGTTGGACATCTTTATTTTTCTTAATGTTCA
 GATACCAATGGACTTGGGAGGAAGAAATTTCTTCCACACCTCAGTTTTTGTACCGCTGG
 CTGCCCAGTAGGAGAGGAGGAGTATCAGGATTTGGTGTGCCCTCTGCTAGCATGAGCGGAGC
 TGCTGATCAGAATGGCGGAGCGGGAGACACAACCTGGGGCCAGGGCTTCCACTTGGAGACC
 AGTGAAGGGGGCGGCTCGGGCAGCGCTCTCTCAAGCCACTTTCCTCCAGTGCTGGGGTG
 CACTTAACAACCTGCGTTCTGGCTAACACTGTGGACCTGACCCACACTGAATGTAGTCTTTC
 AGTACGAGACAAGTCTTCTTAATCCCGAAGAAAATATAAGTGTGCCAAAGTTTTCAGAT
 TCTTCATTCAAGTCTTACTGCTGTGAAGAACAATACCAACTGTGCAAAATGGCAAACTGAC
 TACATTTTTTGGTGCTCTCTCTCTCCCTTTCGCTGGAATATGGGTTTTAGCGGGTCTCT
 AATCTGCTGGCATTGAGCTGGGGCTGGGTACCAAACCTTCCCAAAGGACCTTATCTCTT
 TCTTGCCACACATGCTCTCTCTCCACTTTTCCCAACCCCCACATTTGCAACTAGAAAAGTTG
 CACTTAAAAATTTGCTCTGCCCTTGACAGGTTCTGTTATTTATTGACTTTTGGCAAAGCTGGT
 ACAACAATCATATTACGTTATTTTCCCTTTTGGTGGCAGAACTGTTACCAATGAGGGGAG
 AAGACAGCCACGGATGAAGCGTTTCTCAGCTTTTGGAAATGCTTCAGTCAATCCGTTGTT
 AAGCGTTTGGCACCTCTTCAGATATTTTTATAAAAAAGTACCACCTGAGTTCATGAGGGCCA
 CAGATTTGGTTATTAATGAGATACGAGGGTTGGTCTGGGTGTTTTCTCTGACCTAAGTGA
 TCAAGACTGTAGTGAGTTGACAGCTAACATGGGTTAGGTTTAAACATGGGGGATGCACCCC
 TTTGCGTTTCATATGATAGCCCTACTGGCTTTGTGAGCTGGAGTGTGGTTGCTTTGTGT
 TAGGAGGATCCAGATCATGTTGGCTACAGGAGAGATGCTCTCTTTGAGAGGTCTGGGCATG
 ATTTCCATTTTCAATCTCATTTCTGGATATGTGTTTATGAGTAAAGGAGAGACCCCTATA
 CGCTATTTAAATGTCACTTTTTTGCTATCCCCGTTTTTTGGTTCATGTTTCAATTAATGTT
 GAGGAAGGCGCAGCTCCTCTCTGACAGTAGATCATTTTTTAAAGCTAATGTAAGCATCTTA
 AGGGAATAACATGATTTAAGGTGAAATGGCTTAGAATCATTTGGGTTTGAAGGTTGTGTTA
 TTTTGTAGTCATGAATGTAAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACTTTTTT
 TCGTAGGTGGGCTTTTCTATCAGAGCTTGGCTCATAACCAAAATAAGTTTTTTGAAGGCCA
 TGCGTTTTACACAGTATTTTATTTTATGACGTTATCTGAAAGCAGCTGTTAGGAGCAGT
 ATTGAGTGGCTGTACACTTTTGGGCAACTAAAAAGGCTTCAAACGTTTTGATCAGTTTTCTT
 TCTGAGAAACATTTGCTCTAACAGTATGACTATTCTTCCCACTCTTAAACAGTGTGAT
 GTGTGTTATCTTAGGAAATGAGAGTTGGCAAAACACTTCTCATTTTGAATAGAGTTTGTGTG
 TACTTCTCCATATTTAATTTATATGATAAAATAGGTGGGAGAGCTGTGAACCTTAACTGTGA
 TGTTTTGTGTTTCATCTGTGGCCAAATAAGTTTACTTGTAAATTTTGAAGGCCATTACT
 CCAATTATGTTGACGCTACACTCATTTGACAGGCTGGGAGACTCATTTGATGATGATAAGAA
 TTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGTACCTCTTACAGTCAAGTGCCTGCGAG
 CAGTCATTTTTTCTAAAGGTTTACAAGTATTAGAATTTTCACTCAGGCAAAATGTTCT
 ATGAAGTTATTTCTTAAACATGGTTAGGAAGCTGATGACGTTATTTGATTTTGTCTGGAT
 ATGTTTCTGGAATAAATTTTACCAAAACAAGCTATTGAGTTTGTACTTGACAGGCAAAACA
 TGACAGTGGATCTCTTTACAAATGGAAAAAAAATCCTTATTTTGTATAAAGGACTTCC
 TTTTTGTAAACTAATCCTTTTTTATTTGGTAAAAATGTAAATATAATGTGCAACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVVGKLG LISPAYLFLWPEAFLYRFQIWRPITATFYF
 PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
 LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
 MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFRL
 GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG
 GTAGCTTCTATCCTGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCTACTCCCTCTCGGCT
 CCTTGTGGCCCAAAGCCCTAACCGGGTCCGGCGGTCTGGCTAGGGATCTTCCCGTTGCC
 CCTTGGGGCGGG**ATG**GCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
 CGGGGTTCTGCGAGGCCAGACTGGTCCATCCCCTCTTGGACTTTGTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT
 GGCCTGTGTTCCCTTGTTTTGTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTAGAAGGTTACCTCAAAGAAATTGGAATT
 AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC
 CATTTTGCACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTCGAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCACTGACCTGAACACGAAGAGATGAAATCCT
 GAGGGAAGTTCTTAGAAAAATCAAAAGAGGAATATGACCAGGAAGAAGAAAGGAGAGAAAA
 AACAGTTATCAGAGGCTAAAACAGAAGAGCCCACAGTGCATTCCAGTGAAGCTGCAATAATG
 AATAATTCCCAAGGGGATGGTGAACATTTTGACACCCACCCTCAGAAGTTAAATGCATTT
 TGCTAATCAGTCAATAGAACCTTTGGAAGAAAAGTGGAAAGGTCTGAAACTTCCTCCCTCC
 CACAAAAAGCCCTGAAGATTCCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
 TTATCAGTACTTGGAACAGAAGAAGCTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAAATATGGAGCAGAAAAG
 GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
 CAAACATTACTAAAGAGGAGATTGCTTGACAGAGAACTCAAGAAGAAGTTATTAATAAG**TA**
ATAATTAAGAACAATTTAACAAAAAGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC
 CTTACACTG

FIGURE 6

MAEEEEDEVWVVESIAGFLRGPDWSIPILDFVEQKCEVNCCKGGHVITPGSPPEPVILVACVP
 LVFDDEEESKLTYTEIHQEYKELVEKLLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
 VLAADFETIFKAMMVQKNINEMQLQAIRLIQERNGLPDCLTDGSDVVSLEHEEMKILREVL
 RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
 IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
 MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLLKRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
 TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
 TTAATGAAGATCAATTTCAAGAAGCATGCACCTCTCCTCTTGCAAAGACCCATACATCACAG
 GCCATTTTGCACCTGTGTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
 AGAAAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTTATTA
 CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAAT
 CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA

FIGURE 8

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTG
 TAGCTTCTCCAGCTATGGACCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGTGGCTTCTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAGAAAC
 AGTGGAATGGAAAAACAGTGTAGTCATCTGTAATATGCTCCCTGTCAACCAATGTATAC
 ATTCCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAAAGTATGATTATCTTCCAACCTACTGTGAATGTGTGCTCAGAACTG
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAG
 AAATTTGAAATATGCTTCTGGAAGGAATTCCTGATTTCATGAAGTGGTCCATTCCTGCCT
 TTCTTTATTTCTGGATAAATCTGATTGTCTTCTATGTCTCTGCTATCTTCAACCAGCCATG
 GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTACGAGTAGTGCTGAA
 GAGGCGCTCAAACCTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTGTCTATTGTGGCCT
 TGACTGCCGGGACTAAAACCTTTACAGCAAACTTGGCAGGACGTGGATTTTCATCAGTAGCC
 TTTTTCAGCCCTTCCAATTCCTGCCTTCTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTG
 TACAGCAAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTCAGTC
 ACATCCGCTCTGGCATTGGGCAATGTTCTTATATAGTCCAGTGTTTTATTTCTTCAATGGCT
 AATATCTATATAAGAAAGTACTAGTGAAGGAGGGGAACAGCTCACTGAAAGCAATCTTCATACA
 GAACAGCAAACTCTATTCTTTGGCATTCTGTTAATGGGCTGACTCTGGGCCCTTCAGAGGA
 GTAACCGTGATCAGATTAAGAAGTGTGGATTTTTTATGGCCACAGTGCATTTTCAGTAGCC
 CTTATTTTGTAACTGCATTCCAGGGCCTTTCAGTGGCTTTTATTCTGAAGTTCCTGGATAA
 CATGTTCCATGCTTGTAGTGGCCAGGTACCAGTGTCTATTACACACAGTGTCTGTCTGG
 TCCTTGACTTCAGGCCCTCCCTGGAATTTTCTTGGAAAGCCCATCAGTCTTCTCTCTATA
 TTTATTTATAATGCCAGCAAGCTCAAGTTCGGGAATACGCACCTAGGCAAGAAAGGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCAGTGGGGATGGAGAAGAACTAGAAAGACTTA
 CCAACCCCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGCA
 GCTCTCTGAACCTTATTTTCAATTTTCAGTGTGTGTAATATTTATCTTTTCACTTTGATA
 AACCAGAAATGTTCTAAATCCTAATATTCTTTCATATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATCTTAAAGAACTGATACAGGAGTAACA
 ATATGAAGATTCTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTTGGCCTTCAAGCTTCCAAAAAACTTGTAATAATCATGTTAGTATAGCTTGATAT
 ACACATAGAGATCAATTTGCCAAATATTCACATCATGTAGTTCTAGTTTACATGCCAAAGT
 CTTCCCTTTTTTAACATTATAAAAGCTAGGTTGTCTCTTGAATTTTGGAGGCCATAGAGATAGT
 CATTTTGAAGTAAAGAGCAACGGGACCCTTCTTAAAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTTGGATGATGTAGTCTGTGCTAAATATTTTGTCTGAAGAAGCAGT
 TTCTCAGACACAACATCTCAGAAATTTAAATTTTGAAGAAATCATGGGAAATGGATTTTTGT
 AATAATCTTTGATGTTTTAAACATTGGTTCCTAGTCACCATAGTTACCACCTTGTATTTTA
 AGTCATTTAAACAAGCCACGGTGGGCTTTTTCTCCTCAGTTTGGAGGAAAAATCTTGAT
 GTCAATAGCTCTGAATTTATCATTTTGGAGAATAAGAGGGCATTTTATTTTATAGTTACT
 AATTCAAGCTGTGACTATTTGTATATCTTTCCAAGAGTTGAATGCTGGCTTCAGAATCATAC
 CAGATTGTGCTGAGTGAAGCTGATGCCTAGGAACCTTTTAAAGGGATCCTTTCAAAGGATCATT
 AGCAAAACACATGTTGACTTTTAACTGATGATGAATATTAATCTCTAAAAATAGAAAGACC
 AGTAATATAAAGTCACCTTTACAGTGTACTTCACTTAAAGATGCAATGGTATTTTTCAGT
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAA
 AAATTAGCAAAACAAAGTGACTTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGG
 CTTTAACTGGCAGCCGTGATGTTTACAGACTACCATGCTGAATATGAGCTTTATGGGTGT
 CATTTCTCAGAACTTATACATTTCTGCTCTCCTTCTCCTAAGTTTCATGTCAGATGAATATA
 AGGTAATATACTATTATATAATTCATTTGTGATATCCCAATAATATGACTGGCAAGAATTG
 GTGGAAATTTGTAATTAATAATTTATTAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLPGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
 LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAV
 IFSNFSIITALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
 SPNSNCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI
 FVTAFAQGLSVAFILKFLDNMFHVLMAQVTTVIIITTVSVLVDFRPSLEFFLEAPSVLLSIFI
 YNASKPQVPEYAPRQERIRDLGSLWERSSSGDGEELERLTTPKSDSEDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
 298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAACAGTGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACAATGTATACATTCTGCTAGG
TGCCATATTCAATGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACACTACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCCTGTCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGTGAAGAGGCGTCTAAA
CTGGATCCAGTGGGCTTCCTCCTGACTTTATTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAAACCTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCGGCTTGCTAGCGCGCGGCGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCCCTGCGGGGCGAGGAGCAT
 CCCGCTTACCAGGTCCTCAAGCGGCGTGGCCCGCGGGTCATGGCCAAAGGAGAAGGCGCCGAG
 AGCGGCTCCGCGGCGGGGCTGCTACCCACAGCATCCTCCAAAGCACTGAACGCCCGGCCCA
 GGTGAAGAAAGAACCGAAAAAGAAACACAGTTGTCTGTTGCAACAGCTTTGCTATG
 CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCTGGGTTTCTTCCCTCAGATCTAC
 CTATTG**CATG**TGGCTCAGGTGGGCCCCCTTCTCTGCCTCCATCATCCTGTTTGTGGGCCGAGC
 CTGGGATGCCATCAGACCCCCCTGGTGGGCTCTGCATCAGCAAAATCCCCCTGGACCTGCC
 TGGGTGCGCTTATGCCCTGGATCATCTTCTCCACGCCCTGGCCGTCATTGGCTACTTCCTC
 ATCTGGTTCGTGCCGACTTCCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCT
 CTTTGAACAATGGTCACGTGTTTCCATGTTCCTACTCGGCTCTCACCATGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGGACAAATCGTGGGCCAAGCAGACACGCCCTTGTTCAGG
 ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAACCATACACATGGCACCACCTTCACAC
 AGGGAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGCTGTATCTATATAATCTG
 TGTGTCTATCCTGATCCTGGGCGTGGCGGAGCAGAGAACCTATGAAGCCAGCAGCTCTG
 AGCCAATGCGCTACTTCCGGGGCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCT
 ATTACTGGCTTCTCTTCCCTCCTTGGCTTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCTGGCCATCATGCTCT
 CGGCCACTTTAAACCATTCCCCTCTGGCAGTGTTCTTGACCCGGTTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATATTACATATCGGCTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC
 TACCCTGGTCCATGCTGCCTGATGTCTATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTTCTCTTCTATGTCTTCTTACCAAAGTTTGCCCTCTGGAGTGT
 ACTGGGCAATTTCTACCCTCAGTCTGGACTTTGCAGGGTACCAGACCCCTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCTG
 CTGGGCTGCTGCTCTTCAAAATGTACCCATTGATGAGGAGAGGCGCGGCAGAAATAAGAA
 GGCCCTGAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCCTCT**TAG**GGGCCGCCACGTTGCCGGAAGCCACCATGCAGAAGGCCACAG
 AAGGGATCAGGACCTGTCTGCCGGCTTGTCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGGAGTGGCCAGGACACTTGCTGTGCTCACTGTGGGCGCGGCTGCTCTG
 TGGCCCTCTGCTCCCCCTCTGCTGCTGTGGGGCCAAAGCCCTGGGGCTGCCACTGTGAATA
 TGCACAGGACTGATCGGGCTAGCCCGGAACACTAATGTAGAAACCTTTTTTTACAGAGCC
 TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGTCTGTGAGCTA
 TTAATGTTATTAATTTTCATAAAAGCTGGAAGC

FIGURE 12

MWLRWALS LPPSSCLWAE PGMPSQT PWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
 SCPTSHTARPIGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
 GTAIQGQIVGQADTPCFQDFNSSTVASQSANHTGTTSHRETQKAYLLAAGVIVCIYIICAV
 ILILGVREQREPYEAAQQSEPIAYFRGLRLVMSHGPIYIKLITGFLFTSLAFMLVEGNFVLFCT
 YTLGFRNEFQNL LLAIMLSATLTIPWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
 ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG
 ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQNKAL
 QALRDEASSSGCSETDSTELASIL

FIGURE 13

GGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTGT
 GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
 GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
 TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGTTT
 TGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCTC
 GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
 TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
 CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
 ACCCTGGTCCATGCTGCCTGATGTGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
 GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
 ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAAACAGAAAACCTGTTAGAAATG
 GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
 CAGTTTTATGCATTGCTACCATTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCTGAA
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGAATACTGAGTTGTTTAGG
 ACTTTCTATTGTGGCAAACCTCCAGAAAACAACCCCTTTTGCTGCACATGTAAGTGGAGCTG
 TGCTTACCTTTGGTATGGGCTCATTTATATATGTTTGTTTCAGACCATCCTTTCTACCAAATG
 CAGCCCAAAATCCATGGCAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
 AGTAAGTGCACCTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG
 ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
 ACTGCAGCAGAATGTTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
 TTTTCAGAAAATTTCTTACGGGTGGAAGCCAATTTACATGGATTAAACCTCTATGACACTG
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCAGAGATATTTGAAGAAAGGAT
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAAGTTGCTTA
 TTCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTTCTAAAGGATATCATCAAGAAGACTA
 TTA AAAACACCTATGCCTATACTTTTTATCTCAGAAAATAAAGTCAAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFIIFSITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
 AAVLCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
 AVLTFGMGSLYMFVQTIILSYQMOPKIHGKQVFWIRLLLVIIWCGVSALSMLTCSSVLHSGNFG
 TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFSGFFLTYYIRDFQKISLRVEANLHGLTLYD
 TAPCPINNERTRLSRDI

FIGURE 16

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
 TCCGCTCTCTCGGGTCTTTTCCTGGTCCCAGGCCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
 GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGGTGAAGCAGT
 TACCAAGAATCTTCAACCCTTTCCACAAAAGCTAATTGAGTACACGTTCTCTGTTGAGTACA
 CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
 GTTGTAACAGAAAACTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
 TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
 CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCCGCCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCGCGGG
 CCGGGGTGCGGAGCCGACATGCGCCGCTTCTCGGCTCCTTCTGGTCTTCGCCGGTGCAC
 CTTGCGCTTGTACTGTGCTGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCGTGTGGTTCCCTCCGACCTGGCAGAGCTGCCGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTTCTGCTCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTGCCATCCCGGCTCCAGCTTCTGAATGTTTTAGCTGGTGCCT
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTCTCTGATAAAGT
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTGTGTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCATGACACCAAACTGGTTCTTGAACCTCTCGGCCCCAATTCTGAACATT
 CCCATCGTGCAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAATTTTCATCTGTGT
 GCAGACAGGGTCCATCTCTGTCAACCTAACCTCTCTGGATGCTCTTTTTCTCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAATTCCTGGAACCCCTCATTAAAAAATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGA
 CACATGACTGGATTTTCTGTTTGGCACATCCCTGGACTCAGTTGCTTATTTGTGTAATGGA
 TGTGGTCTCTAAAGCCCTCATGTTTTTGATTGCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGATTACATCAGGT
 TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGT
 GGCCGGGCGCGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTCT
 ACAAGGTCAAGAGTTCAAGACCAGCCTGGCCAAGATGGTGAATCCTGTCTCTAATAAAAAAT
 ACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGAGGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCCT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRElseVIREYR
KEHQAYVFLFLFCGAYLYKQGFAIPGSSFLNVLAGALFGPWLGLLLCCVLTSVGATCCYLLSS
IFGKQLVVSYPFDKVALLQKQVEENRNSLFFFLFLRLFPMTPNWFLNLSAPILNIPIVQFF
FSLVIGLIPYNFICVQTGSILSTLTSLDALFSWDTVEKLLAIAMVALIPGTLIKFKFSQKHLQ
LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCGAGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAACGCCAGCTCAGAA
 TAGGAAAAATACTTGGGATTTTATATTGGAAGACATGGGATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAACTTTCAGAGACTGTTGATTGGTGAGACAGACCGGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAAATGAACCTCAGAGACC
 CCCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCCATTAGCACCTGAGCCAGTGCCTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGCTCTTGCCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCTCTGCATGGGGTGATGAAGACAGACCCCTTTC
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCC
 AACTGCACTGGCTGTGCCCAGAAACACCTGAAGTGATGCTCCTGGAAGACGCCCCAAGGAA
 ATTTGACAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCCTGTTGGAGGAAGAGATT
 AGCATTTTTTGTGCCAGTACCTTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTTCTGAGCGGTGGTCCCATTTCCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTGAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTGCG
 ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
 GGAACCGCTTTCTCAGAACTGTAGGAAATAGAAGTGTGCACAGGAACAGCTTCCAGAGCCGA
 AAACCAGGTTGAAAGGGGAAAAATAAAAAACAAAACGATGAAACTGCAAAAA

FIGURE 20

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFTRQLLEKNEPQRPPPYPLLIVVY
 KVLATLGLILLTAYFVIQPFSPLAPEFVLSGAHTWRSIIHHIRLMSLPIAKKYMSENKGVPL
 HGGDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
 GKPLLEEEIQHFLCQYPEATEGEFSEGGFFAKWWRFCFPERWFFPYPWRRPLNRSQMLRELFV
 FTHLPFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCSVAMP
 IEPGDIGYVDTHWKVYIARGVQPLVICDGTAFSEL

$\begin{pmatrix} a_{11} \\ a_{12} \end{pmatrix}$
 $\begin{pmatrix} a_{11} \\ a_{12} \end{pmatrix}$
 $\begin{pmatrix} f_1 \\ f_2 \end{pmatrix}$
 $\begin{pmatrix} g_1 \\ g_2 \end{pmatrix}$
 $\begin{pmatrix} h_1 \\ h_2 \end{pmatrix}$
 $\begin{pmatrix} i_1 \\ i_2 \end{pmatrix}$
 $\begin{pmatrix} j_1 \\ j_2 \end{pmatrix}$
 $\begin{pmatrix} k_1 \\ k_2 \end{pmatrix}$
 $\begin{pmatrix} l_1 \\ l_2 \end{pmatrix}$
 $\begin{pmatrix} m_1 \\ m_2 \end{pmatrix}$
 $\begin{pmatrix} n_1 \\ n_2 \end{pmatrix}$
 $\begin{pmatrix} o_1 \\ o_2 \end{pmatrix}$
 $\begin{pmatrix} p_1 \\ p_2 \end{pmatrix}$
 $\begin{pmatrix} q_1 \\ q_2 \end{pmatrix}$
 $\begin{pmatrix} r_1 \\ r_2 \end{pmatrix}$
 $\begin{pmatrix} s_1 \\ s_2 \end{pmatrix}$
 $\begin{pmatrix} t_1 \\ t_2 \end{pmatrix}$
 $\begin{pmatrix} u_1 \\ u_2 \end{pmatrix}$
 $\begin{pmatrix} v_1 \\ v_2 \end{pmatrix}$
 $\begin{pmatrix} w_1 \\ w_2 \end{pmatrix}$
 $\begin{pmatrix} x_1 \\ x_2 \end{pmatrix}$
 $\begin{pmatrix} y_1 \\ y_2 \end{pmatrix}$
 $\begin{pmatrix} z_1 \\ z_2 \end{pmatrix}$

FIGURE 21

CCACGGTGTCCGTTCTTCGCCCCGCGGCAGCTGTCCCCGAGCGGGAGGAGCCCCAGGGGCG
 CGAGCCCCGCATGAATCATGTAGTCAATCATTTTCCAGTTCTCAGCCGTTCA GTTGTGATC
 AAGGGACACGTGGTTTCCGAAC TGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
 GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAACTTT CAGAGACTGTTG
 ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTATC
 AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
 TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
 CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

FIGURE 22

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCTCCTGGCTGGTG
 CCCTGCTGGCCACCTGCTAGACCGTGGCTTATGAGCCGCTGGGGTGCAGTGGGACTGCC
 CTCCTCGCCACCACCAATGGCAGCCCCACCTTCTTTGAAGACTTCCAGCTTTTTGTGCCA
 CACCCGAATGGCCGCACTTCGACAAACAGCTACAGCCAACTGTCCAGTTCGAAATG
 GACACGTATGCTAAGAGCCACGACCTTATGTCAGGTTTCTGGAATGCTCTGATGACATGCT
 TATGAGCAGTGGGCGAGCGCCAGTGGGAGCGCGCCAGAGCTCGTGGGGCTTCTCCAGGAGC
 TGGTGTGGAACCTGCGCAGAGGCGGGCGCGCCTGGAGGGGTACGCTACACGGCAGTGTCTG
 AAGCAGCAGCAACGACCACTCCATGGCCCTGCTGCACTGGGAGGGCGCTGTGGCGGAGCT
 CGCCAGCCCATGTGGGGCTGGCGCTGAGGGACACTCCCATCCCCGCTGGAACACTGTCCA
 GGCCGAGACATATTCCAGCATGCGTCTGAAGCTGGTGCCCAACCATCACTTGCACCTGCAC
 CTGGAAGCCAGCGCTCTCGAGACAATCTGGGTGAGGTTCCCTGACACCCACCAGGAGGCG
 CTCACTGCTCTGGCAGTGACCAAAGAGGCCAAAGTGAGCACCCACCTCGAGTTGCTGCAGG
 AGGACCACTGCGGAGGACGAGCTGGCTGAGCTGGAGACCCCGATGGAGGCAGCAGAAGTGTG
 GATGAGCAGCGTGAGAAGCTGGTGTCTGCGCCGAGTGCCAGCTGGTGACGGTAGTGGCCGT
 GGTCCCAGGGCTGTGGAGGTCACCAACAGAATGTACTTCTACGATGGCAGCACTGAGC
 GCGTGGAAACCGAGGAGGCTACGCGCTATGATTTCCGGCCCACTGGCCAGCTGCGTGAG
 GTCCACCTGCGCGCTTTCAACCTGCGCGCTTACAGCACTTGAGCTCTCTTTATCGATCAGGC
 CAACTGCTTCTCAACTTCCCATGCAAGGTGGGACGACCCAGCTGCTACTCTTAGCCAGA
 CTCGAGACCCGAGCTGGCCCATCCCAACCCATACCCAGGTACGGAACCAAGTGTACTCG
 TGGCTCTGCGCCCTACGGCCGCCCTCTCAAGGCTTACCTAAGCAGCGCTCCCCAGGAGAT
 GCTGCGTGCTCAGGCTTACCAGAAATGGGTACAGCGTGAGATATCCAACCTTCGAGTACT
 TGTATGCACTCAACACCATTTGCGGGGCGGACCTACAAGTGTCTGCTACGATCTGTGTTCT
 CCCTGGTCTCTGAGGACTACGTGTCCCCAACCTTGGACCTCAGCAACCCAGCGCTCTCCG
 GGACCTCTCTAAGCGCTACGCTGTGGTGAACCCCAAGCATGCCACGCTCGTGAGGGGAAAGT
 ATGAAAGCTTTGAGGACCCAGCAGGAGGACCATTGACAAGTTTCACTATGGCACCCACTACTCC
 AATGAGCGGCGTGTAGCACTACCTCATCCGCGTGGAGCGCTCACTCCCTCAGCTGCCA
 GCTGCAAGTGGCGCTTTGACTGCTCCGACCGGCGAGTTCACCTCGGTGGCGGAGCGTGGC
 AGGCAGCGCTGGAGAGCCTGCCGATGTGAAGGAGCTCATCCCGGAATTTCTTCACTTTCTCT
 GACTTCTTGGAGAACCAGAACGCTTTTGAACCTGGGCTGTCTCCAGCTGACCAACGAGAAGGT
 AGGCGATGTGGTGCTACCCCGTGGGCGAGCTCTCTGAGGACTTCATCCAGCAGCAGCGCC
 AGGCTCTGGAGTCGGAGTATGTGTCTGCACACCTACAGAGTGGATTCGACCTCATCTTTGGC
 TACAAGCAGCGGGGGCGAGCCGCGGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTTAGA
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA
 TCAGCAACTTTGGGCAGACTCCCTGTGACGTGCTGAAGGAGCCACATCCAACCTCGGCTCTCA
 CCTGGAGGAACGAGCCCATCGCCTTGCACGCTGGACACTAATCACTACGATCTTCCAGCA
 CGTGGAGCAACTCAAGGCATTCTTCGCAAGGTAAGTGTGAGTGCCAGTGGGCTGTCTGGGCA
 CCCACAGCTGTTGCCCTATGACCGCAACATAAGCAACTACTTCACTTACGCAAAAGACCCC
 ACCATGAGCAGCCACAAGAGCGCAGGCACTGCTGAGTGCCCGTGGGTGCCAGGCACTGGTGT
 GAGTGGACAAGCACTGGCAGTGGCCCCGGATGGAAGCTGCTATTGAGCGGTGGCCACTGGG
 ATGGAGCGCTCGGGGTGACTGCACCTACCCCGTGGCAAGCTGTTGAGCGAGCTCAGCTGCCAC
 CTTGATGTAGTAACCTGCTTGCACCTGGAACACTGTGGCATCTACCTCATCTCAGGCTGCCG
 GGACACCAACGCTGATGGTGTGGCGGCTCCATGCATCAGGTTGGTCTGCTGAGGAGCTGGC
 CAAAGCTGTGCGAGTCTGTGTATGGGCTATGGGGCTGCACTGAGCTGTGTGGCCATCAGCAT
 GAACCTGACATGCTGTCTGTGATCTGAGGATGGAAGTGTGATACAGACACTGTACGCGC
 CGGACAGTTTGTAGCGGCACTACGGCTCTGGGTGCCACATTCCTTGGGACCTATTTTCCACC
 TGGCATTTGGGTGCCAAGGCCAGATTGTGGTACAGAGCTCAGCGTGGGAAGCTCTGGGGGCG
 CAGTCACTACTCTTGCACCTGTATTGAGTCAATGGGAAGTGTGGGGCTTCACTGGCCCCCT
 GGCAGAGCACTTACGCGCTGACGGTGACAGGAGCACTTTGTGTTGCTGGGACAGCGCCAGT
 GCGCCCTGCACATCTTCAACTAAACACACTGCTCCGCGGCGCGCTCCTTGTGCCATGAAG
 GTGGCCATCGCAGCGTGGCGGTGACCAAGGAGCGCAGCCAGTGTGTTGGGCTGGAGGA
 TGGCAAGCTCATCTGTGTTGGTGCAGGGGAGCCCTCTGAGGTGGCGAGCAGGCACTGCGCG
 GGAAGCTGTGGCGGTCCTCGCGCGCATCTCCAGGTTCTCTCGGAGAGACGGAATAACA
 CCTACTGAGGCGCGCTGCAACTGGCCAGTCCGGCTGCTCGGGGCCCCCGCCCCGAGGCGCTG
 CCGCGGAGGCCCCGCCAGAAGTCCGCGGGAACACCCCGGGGTGGGACCGCCAGGGGGTGA
 GCGGGGGCCCCAGCTGCCAGCTCAGGATTGGCGGGCGATGTTACCCCTCAGGAGATTGGCG
 GCGGGAAGTCCCCCGCTGCGCGGCTGAGGGGCGCGCTGAGGCGCAGCACTGGCGCTT

FIGURE 23

MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELALETP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPPIPPHTQV
 RNQVYSWLLRLRPSPQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDSCDRQFHSVAAAWQARLESAPADVKEIP
 EFFYFPDFLENQNGFDLGLCLQLTNEKVGDVVLPWASSPEDFIQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAEEALNVFYCTYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTQRLLSGPWPVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRVTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYILISGSRDTCMVWRLRHQGGLSVGLAPKVPQVLYGHGAAVS
 CVAISTELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPFIHFLALGSEGQIVVQSSA
 WERPGAQVITYSLHLYSVNGKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTEAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
 CACGCCCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
 CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAATCTATGGGGTCTGGGGCTCTTC
 TGGACCCCTTAATGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCTTTGCCCTCCTT
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCCTTAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACACTGGGTCATTGGCATTGGAGCCCTCATCTGACCCCTGTGCGAG
 ATAGCCCCGGTTCATCTGGAGTATATTGACCACAAGCTCAGAGGAGTGCGAACCCTGTAGC
 CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
 AATGCGTTCATGCTACTCATGCGAAACATTGTGAGGGTGGTCGTCTGGACAAAGTCACAGA
 CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGTCTGTCTCTCTTTT
 TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAGACTTTAAGAGCCCCACCTCAACTATTAC
 TGGCTGCCCATCATGACCTCCATCCTGGGGGCTATGTCATCGCCAGCGGCTTCTTCAGCGT
 TTTGCGCATGTGTGTGGACACGCTCTTCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
 GAGGGCCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGGCCCTGATCCAGGACTGC
 ACCCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
 AAAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCCTGTAATCCAACACTTTGAGAGGCTG
 AGGCGGGCGGATCAGCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC
 GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTATCCAGCTAC
 TCGGGAGGCTGAGGACAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
 AAAGATTTTATTAAAGATATTTGTTAACCT

[illegible]

FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCAGCGCCAGGCGTCCGGCCGCCGT
 GGC**TATG**TTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCGCTGTTC
 CAGTGTGACCAGCTGCAATATACGCTGGTTCAGTTCCTGGGTGGCAAGAACTTGAAACTGC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG
 CCAGTCAATGTGTCATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCGCCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGGTGAGGCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCGGCGAGAGTGGGAGGCCCCGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAAGAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTTGCAGCG
 CCACGTTTCCCGCCACAACCAACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGCTTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCCTTGACAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTC
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAAATAAA
 TTTGGGATGAAGGACATGCGCGTGACAGCTTTCAGCATTCATTTTGGGTCAAGCACAAAGTT
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAACTCGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTTGCCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGGCTTTCTGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTGATGCTGTCTCTTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACCTGCTCA
 AGTCCCTTGTGTGTTCGACAAAGAACCGGCGCTGCAAACCTGCTGCCCTGGTGATGGCTGCC
 CCCCTGAGCATGGAGCATGGCAGAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGA
 TGCTGCACAACCATTTTACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCACTTATTTCCCTCCTGTCC**TAG**GAAATTGATTCTTCCAGAATGACCTTCTTATT
 TATGTAAGCTGGCTTTCATTTAGATTGAAGTTATGGACATGATTTGAGATGTAGAAGCCATT
 TTTTATTAATAAAATGCTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCANVDLLDILQPEDDTIFFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAIEDIFRDEEEDEEHSGNDSGSEPSEKTRLEEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLRH
VSRHNRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSLNTSYTAARFKLWSVHGQKR
LQEF LADMGLPLKQVKQKFQAMD ISLKENLREMIEESANKFGMKDMRVQTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLSKHLKSFVCSTKNRRCKLLPLVMAAP
LSMEHGTVTTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFL
DALISLLS

FIGURE 28

GTACCTCAGCGGAGCGCCAGGCGTCCGGCCCGCTGGCTATGNTCGTGTCCGATTTCGCA
 AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCTTCTCTCGTGGCCTCGGANGTGGAT
 GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
 GGTTCAGTTTCTGGGTGGCAAGAAGTGAAGTGCATTTCTTGAGCATAAAGAACAGTTTC
 ATTATTTTATTCTCATAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
 GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
 CGATACCC

FIGURE 29

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTCTAGTGAAC
 CACGAAGGGAGCATACAGAAAAACACCCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG
 GCTGACTTTGGCTATAGAAAAAGAAAGGAACGAAAGAGACAGTTTTTTTGGAAAGCTAA
 GTCTTCCTCTTATCCAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAAACAAT
 GAGTAAAGTAGCTCCGTCAAC**ATG**TGTGACAGCGCCCTGGGTCCCTGTGGGACGGCTC
 CTGCTCTTTTCTCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGC
 CAGCGGCTGCCAACGGTGTCTGACTCTGAGGACCCCTGGATCTGCCACTGTATCCTCAG
 CCTCTTCTCCGGCCGCCCCACGCGCTGCTGAGATCAGACCTTACATTAATATCACCATCT
 CTGAAGGGTGACAAAGGGACCCAGGCCAATGGGCCCTGCCAGGGTACATGGCGAGGGAGGG
 TCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCG
 GCGCCCGTGCCAGAAAGCCTTCTTCGCCCTTCTCAGTGGGCCCAAGACGGCCCTGCACAGC
 GGGGAGGACTTCCAGACGCTGCTCTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGGCACCGGCCAGTTTGTCTGCTCCCTGCGGTGGCATCTACTCTTACAGCTCAATGTGC
 ACAGCTGGAATTACAGGAGACGTACGTGCACATTATGCATAACAGAAAGAGGCTGTCACT
 CTGTACGCCAGCCAGCCAGCGACGACATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGGGACCGGCTCTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAAGCCACTTACAGCA
 ACGACTTCGACACCTACATCACCTTCAAGGCCACCTCATCAAGGCCAGGACGAC**TG**AGGG
 CCTCTGGGCCACCCCTCCCGGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTGCAGGGCTCAG
 TTTGCACTGCTGTGAAGCAGGAAGGCCAGGAGTCCCGGGGACTGGCATCTGGGAGA
 CCGTGCTTCTATCTTGGCTGCCATCATCCCTCCAGCCATTTCTGCTCCTCTCTTCTCTCT
 TGGACCTATTTTAAAGAACTTGCTAACCTAAATATTAGAACTTCCAGACCTCGTAGGCC
 AGCACTTCTCAAATTTGGAATGCATGCAATACCCGGGGTTCGTGTTAAATCGAGATTCT
 GACTCAGAGGTCTGAGTGGGTCCAGGATTCTGTGTTTCTCATATGTTCTGGGTGATGCTG
 ATGGGGTCAGTCTATGAACCACTGGAGCAACAGGTTCTAGGACTTCTCAATATTCTTAG
 TAGTTTCTGAACATTCTGGAATCTCCACATTTCTAGAATTTCCCAACATTTTTTTTTTCT
 TGACACAGAGTCTTGTCTGTGTGCCAGGCTAGAGTGCAGTGGTGCATCTCAGTTCACTGC
 AAGCTCTGCCCTCCCGGGTTCAAGCGATTCTTCTGCTCAGCTCCCTAGTGGCTGGGATTAC
 AGGCGCTGCTACCATGCTGGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTCCACATA
 TTGGCCAGGCTGGTCTTGAACCTCTGACTTCAGGTGAGCCACCGCCCTCGGCTCTCAAAAT
 GCTGGGATTACAGGTGTGAGCCACCGTGCCTGGCCAATTCCAACATTTCTAAATTTCTCTCAT
 CCTCCAGGGCTCCCGTGCTATGTTCTCTTACCCCTTCCCGCTCTTCTCTTGTCTAGGCC
 TGCACCACTGCAGCCACCGTTTATTATTATTATTATTAACACTGAGCACTCACTCTGTGCT
 GGGTCCCGGAAGGGTGAGGGGGTCAGACACAGGCCCTGCCCTGCCCTCAGTCACTGGCCA
 GTCCAGCCCAGGCGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCCAGAGCTCATGGGG
 GCCTGTGTTCTGGGTGTTGAGTGTCTGGTCTCCATTACCCACTGCTGCTCAAGGCTGG
 TGGGACGGGGTCCCGGTGGCAGGGGAGGTATCTCCTTCCCGTTCCTCATCCACTGCCCGC
 TGCTCATCGTTACAGCAAAACCCAGGGGGCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG
 ACCCAGGAGTGTGGGGGCTATTTGGGGGGTGAAGTGGCCCGGGAAGAAATGGAACCCACACCCA
 TAGCTCTCCCCACAGCTGATACGGCATCTCTGCGAGAAGACCTGCCCTCCTCACTGGGATCC
 CTTCCTGCTCTCTCCAGGGCTCTGCCAGGGCCTTGCTCAGTCCCTTCCACCAAAGTCATCT
 GAACTTCGGTTTCCCGAGGGCTCTCAGCTGCCCTCAGGACCTGCTGTCTCCCAAGGTGCT
 CTCTGCCCTCATGCCCTCTCACCAGGCCAGTCCCCGACTCTCCAGGCTTTATCAAGGTG
 CTAAGGCCCGGGTGGGCAGCTCCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
 AAACACCTCGAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGAGGCTCAGCAGGTCTGGGG
 AGCTAGAGCAAAAGGAGGACCTCAGGCCCTCCGTTTTCTTCTTCCAGGGTGGGGTGGCTGGT
 GTTCCCTAGCCTTCCAACCCAGGTGGCTGCCCTTCTTCTTCCAGGGGAGGGCGGCTCCGC
 CCATTTGCTCATGACGACTCTGGGGCTGAGGTGCCCGGGGGGTGATCTCTGCTGCTCAC
 AGGCCAGGGAGCCGTGGCTCCATGGCCAGATGACGGAACAGGGTCTGACCAAGTGGCCAG
 AGACCTGTGCTATAAACACCCCTGCCTGATCTCTGCCCTGCTGACCCGCGCACGCCCTGCC
 GTCCAGCATGATTAAGAAATGCTGTCTCCTTGGAAAAAAGAAAAA

FIGURE 30

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPH
ALPEIRPYINITILKGDGDPGFMGLPGYMGREGPQGEFGPQGSKGDKGEMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLEFVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAAGCGAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTG
 AGGCGCGCGCTGCCCGCCCGGCTCCCTGCGCGCCCGCGCTCCCGGGACAGAAGATGTG
 CTCACGGGTCCCTTGCTGCTGCCGCTGCTCTGCTACTGGCCCTGGGGCTGGGGTGCAGG
 GCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGG
 ACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAAGGGCAT
 CACCATGCTCGAGCGAGGCAGCTTTGCCGGCCTGCCGGGCTGCAGCTCCTGGACCTGTAC
 AGAACAGATGCCAGCCTGCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTG
 GACCTGACGGGCCAACAGGCTGCATGAAATCACCATGAGACCTTCCGTGGCCTGCGGCGCT
 CGAGCGCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGC
 TCGACCGCCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCCCGTGC
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCAT
 CCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG
 AGGGGCTCTTCAGCCGCTTGCCCAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAG
 CGAGTGCCACCTGTGATCCGAGGCTCCGGGGCTGACGCGCTCGGGCTGGCCGGCAACAC
 CCGCATTCGCCAGCTGCGGGCCGAGGACCTGGCCGGCCTGGTGCCTGCAGGAGCTGGATG
 TGAGAACCTTAAGCTGCAAGCCCTGCTGGCGACCTCTCGGGCCTCTTCCCGCGCTGGG
 TCTGCTGGCAGTGCCTGACCCCTTCAACTGCGTGTGCCCTGAGCTGGTTTGGGCCCTG
 GGTGCGGAGAGCCACGTCACTGCGCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCA
 AGAACGCTGGCCGGTGCTCCTGGAGCTTGACTACGCGCACTTTGGCTGCCAGCCACACAC
 ACCACAGCCAGTGCACCCACACGAGGCGGTGGTGGGGAGCCACAGCCTTGTCTCTAG
 CTTGCTCCTACCTGGCTTAGCCCCACAGCGCGGCCACTGAGGCCCCAGCCCGCCTCCA
 CTGCCCCACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTC
 AATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTTGTCGCCCGAAGGCTT
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTCA
 CGCCGAGGCCACACGGTCCCTGACCTGGGCATCGAGCCGTGAGCCCGCTCCCTGCGC
 GTGGGGCTGCAGCGCTACCTCCAGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTACCTA
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTGCTGCTG
 AGTACAGGTCACCCAGCTGCGGCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGG
 CCGCGAGGCTGCGCGGAGGGCGAGGGCTGCGGGGAGGCCATACACCCAGCCGCTCCA
 CTCGAACCAACCCAGTCAACGAGCCCGCAGGGCAACTGCGCCTCTCTATTGCGCCG
 CCTGCGCGCGGTGCTCCTGGCCGCTGGCTGCGGTGGGGGACGCTACTGTGTGCGGCGG
 GGGCGGGCCATGGCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCC
 GGAATGGAGGGAGTGAAGGTCCCCTTGGAGCCAGGCCGGAAGGCAACAGAGGCGGTGGAG
 AGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCCTGGCCTC
 CAGTCAACCCCTCCACGCAAGCCCTACATCTAAAGCCAGAGAGACAGGGCAGCTGGGGCCG
 GGCTCTCAGCCAGTGAGATGGCCAGCCCTCCTGCTGCCACACCAAGTAAAGTTCTCAGTCC
 CAACCTCGGGGATGTGTGACAGAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA
 CCTCGGTCTCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGCTCCCAAG
 CGAGTGCCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCACTCCTGGCCGCGG
 GGCCTGCCATGTGCTGGTAAAGCATGCTGGGTCTGCTGGGCTCTCCACTCCAGGCGGA
 CCTCGGGGGAGTGAAGGAAGCTCCCGAAAGACAGAGGAGCAGCGGTAGCGCGCTGTG
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAAACTGGAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATTCTG
 GGAAGATGTTTTTCAAATCTAGAGACAAGGACTTGTTTTGTGAAGACAACAGATGATATG
 AAGGCCTTTTGTAAGAAAAATAAAGATGAAGTGTGAA

FIGURE 32

MCSRVPLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPVRDVPDPDVGlyVFEN
 GITMLDAGSFAGLPGLQLLDLSQNIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
 RLRLYLGNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLLDLSHNSLLALEP
 GILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLHDVSDNQLERVPPVIRGLRGLTRLRLAG
 NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVPLSWFG
 PWVRESHVTLASPEETRCHFPKKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS
 SSLAPTWLSPAPATEAPSPPSTAPPTVGPVPQPDCCPSTCLNGGTCHLGRHHLACLCP
 GFTGLYCESQMGQTRPSPPTVTPRPPRSLTLGIEFVSPTSRLVGLQRYLQGS SVQLRSLRL
 TYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPA
 VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGVAAAYCVRRGRAMAAAAQDKGQVGPAG
 PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFFPGPLQSPHAKPYI

FIGURE 33

GAATCATCCACGCACTGCACTCTGCTGAGAGAGTGAAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATTTTACATATGAGGAAATAAGTGGTAAAACTCCTTGGAAATACAATTGAGACTCATCAG
 AAACATTTTACATATTTTGTAGTATTTGTTATGACAGCAGGGGTGATGCTCCAGAGCTGCCAG
 AAGAAAGGGAACGTATGACCAACTGCTCCAACATGCTCTCAAGAAAGGTTCCCGCAGACTTG
 ACCCGGACCAACAGAGCTGATTTTCTATTAACCTCCTTTTCAACTCCAGAGTTTCAAG
 TTTTCATTCTGTCTCAAACTGAGAGTTTGTATTCATGCCATAACAGAGTTTCAACAGCTGG
 ATCTCAAAACCTTTGAATTTCAACAAGGAGTTAAGATATTTAGATTTTGTCTAATAACAGACTG
 AAGAGTGTAACTTGGTATTTTACTGGCAGGCTCTCAGGTATTTAGATCTCTTTTAAAGTACTT
 TGACACCATGCCATCTGTGAGGAGAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGA
 GTGGGGCAAAAAATCAAAAATCAGATTTCCAGAAAATTGCTCATCTGCATCTAAATACTGTCT
 TTCTTAGGATTCAGAACTCTTCCCTCATTATGAAGAAGGTAGCTGCCACTCTTAAACACAAC
 AAAACTGCACATTTGTTTTACCAATGGACACAAATTTCTGGGTTCTTTTGGGTGATGGAATCA
 AGACTTCAAAAATATTAGAAATGACAAATATAGATGGCAAAAGCCAAATTTGTAAGTTATGAA
 ATGCAACGAAATCTTAGTTTGAAGAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGA
 TTTACTCTGGGACGACCTTTTCCCTTATCTTACAATTTGTTGGCATACATCAGTGGAAACACT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCAACAATTCATTTGACTAC
 TCAAATAGTCTTAATGAGAACTATAAAATGGAGCATGTACATTTACAGAGTGTTTTACATTCA
 ACAGAGATAAATCTTATTTGCTTTTGACCAAAATGGACATAGAAAACCTGACAATCTCAAAATG
 CACAAATGGCACACATGCTTTTCCCGAATTAATCTACGAAATTTCCAATTTTAAATTTTGGC
 AATTAATATCTTAAACAGACGAGTTGTTTAAAGAACTATCCAACCTGCCTCACTGAAAACCTCT
 CATTTTGAATGGCAATAAATCGGAGACACTTTCTTTAGTAAGTTGCTTTGCTCAACACAC
 CCTTGGAAACACTTGGATCTGAGTCAAAATCTATTACAACATAAAAATGATGAAAATTTGCTCA
 TGGCCAGAAACTGTGGCTCAATATGAATCTGTCAATAAATTTGCTGATTTCTGCTCTCAG
 GTGCTTGGCCAAAAGTATTCAAATACTTGACCTAAATAAACAACCAATCAAACCTGTACCTA
 AAGAGACTATTCATCTGATGGCCCTACGAGAATAAATATTGCAATTTAAATTTTCTAAGTCT
 CTCCTTGGATGCACTGATTTTCTGATGAGTCTTCAAGTCTGAAACATTGAAATGAACTTCTTCT
 CAGCCCATCTCTGGATTTTGGTTTCTGAGGCTGCCAGGAAGTTAAACCTATAAATGCGGGGAAGAA
 ATCCATTTCCGGTGTAACCTGTGAATTAATAAATTTTCAATTCAGCTTGAACCATATTCAGAGGTC
 ATGATGGTTGGATGGTCAGAGTTTATACACCTGTGAATACCCCTTAAACCTAAGGGGAACATG
 GTTAAAGACGTTTCATCTCCACGAATTTATCTGCAACACAGCTCTGTTGATTGTCACCATTT
 TGGTTATTATGCTAGTTCTGGGGTTGGCTGTGGCCTTCTGCTGCTCCCACTTTGATCTGGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAAACATGGCAGAGGTTAGGAAAACRAACCCA
 AGAACAACTCAAGAGAAATGTCCGATTCCACGCAATTTATTCATACAGTGAACATGATTTCT
 TGTGGGTGAAGAAATGAATTTGATCCCAATCTAGAGAAGGAAGATGTTCTATCTTGATTGTC
 CTTTATGAAAGCTACTTTGACCTGGCAAAAGCATTAGTGAAATATTGTAAGCTTCATTGA
 GAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTCAGAAATGAGTGGTGCCATT
 ATGAATTTCTACTTTTGGCCACCACAATCTCTCCATGAAATTTCTGATCATATAATTTCTATC
 TTACTGGAACCCATTCCATTTCTATTGCAATCCCACAGGTTATCATAACTGAAAGCTCTCCT
 GGAAGAAAAGCATACTTTGGAATGGCCCAAGGATAGGCGTAATGTGGGCTTTTCTGGGGCAA
 ACCTTCGAGCTGCTATTAATGTAAATGATTAGCCACCAGAGAAATGTATGAATCGCAGACA
 TTCAACAGATTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTGATGAGAACAGATTTGCTC
 ATAAATATCCCACAGTCTTTGGGAAGTTGGGAGCCACATACACTGTTGGGATGTACATTGATA
 CAACCTTTATGATGGCAATTTTGACAATATTATTAAATAAATAATGTGGGTTATTCCTTCATA
 TCAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAAACCTTTCAAGAGTTTATAAGG
 GCTTATGGAAGAAAGGTGTTCTCATCCAGGATTTGTTTATAATCATGAAAAATGTGGCCAGTGC
 AGTGGCTCACTCTTGAATCCCAAGCAATGGGAGGCCAAGGTGGGTGACCCAGAGGTCAG
 GAGATGGAGACCATCTTGCCCAACATGGTGAAACCCCTGTCTCTACTAAAAATCAAAAATTA
 GCTGGGCGTGATGGTGCACGCCTGTAGTCCAGCTACTTGGGAGGCTGAGGCGAGGAGATCG
 CTTGACCCGGGAGGTGGCAGTTGAGTGAGCTGAGATCGAGGACTGCATCCAGCCTGGT
 GACAGAGCGGAGCTCCATCTCAAAAAAAGAAAAAAGGAAAAAATGGAATAACATCC
 TCATGGCCCAAAAATAAGGTCTAATTCATAAATTAATAGTACATTAATGTAATTAATATTA
 CATGCCACTAAAAAGAAATAGGAGTGTATATTTTCTGGTATGGAAGAAAAATTAATTAAT
 GTTATAAATCTATTAGGTTGGTGCAAAACATTTGCGGTTTTGTCATGAAATGGCATTTGAA
 ATAAAACTGTAAAGAAATCTATACCAGATGTAGTAACAGTGGTTTGGGCTCGGGAGGTTTGA
 TTACAGGAGGATTTGATTTCTATGTTGTGATTTCTATAATGTTTGAATTTGTTAGAATGA
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHVSVKLRVLILCHNRIQQDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTCKMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSONLLQHKNDENCWPETVVNMNLSYNKLS
DSVFRCLPKSIQILDNNNQIQTVPKETIHLMALRELNIAFNFLDLPGCSEHFSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFCLHFDLPWYLRMLGQCTQTWHRV
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKISENI
VSFIEKSYKSIFVLSPNFVQNEWCHYEFYFAHNNLFHENS DHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRCKGLEWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

FIGURE 35

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPLP
AGPGEWEERRPQEP RP PKRATKPKKAPKREKSAPEPPPGKHSNKKVMRTKSSEKAANDHS
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRNLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGYEKAYEGG
SELGGWSLGRWTHDGIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRSWKQTQEHPTPTDDHVFRWLAYSAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGI PNAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTL SKTNMARI REIMEKFGKQFVSLPARR
LKLGRKRQRG

FIGURE 37

CTAAGAGGCAAGATGAGGCCCGGCTCTCATTTCTCCTAGCCCTTCTGTTCTCTTGGCCAAGCTGCAGGGG
 ATTTGGGGGATGTGGGACCTCCAATTCACAGCCCGGCTTCAGCTCTTTCCAGGTTGTTGACTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGCTCGGGCTCCAGCTCCAGCCGAGCTTAGGCAGCGAGGTTCTGTGTCCCACTTTGTT
 TTCCAATTTACCGGGCTCCGTTGGATGACCGTGGGACCTGCCAGTGCTCTGTTCCCTGCCAGACCACTCTTC
 CCGTGGACAGAGTGGACGCTTTGGAATTCACAGCTCATGTTCTTCTCAGAAGTTTGAGAAAGACTTTCTAAA
 GTGAGGGAATATCTCCAATTAATAGTGTGTATGAAAAGAACTCTTAAACCTAACTGTCCGATATGACATCAT
 GGAGAAGGATACCATTTCTTACACTGAACCTGACTTCGAGCTGATCAAGCTAGAAGTGAAGGAGATGCAAAAAC
 TGGTCATACAGCTGAAGGAGAGTTTGGTGGAGCTCAGAAATGTTGACCACTGGAGCTGGAGATAGAAT
 ATGACTCTCTTGGTAGAGAAGCTTGAGACACTAGACAAAACATGTCTTGGCATTCGCCAGAAATCCTGGC
 TCTGAAGACCAAGCTGAAGAGTGTGAGGCTCTAAAGATCAAAACACCCCTGTCTGTCACCCCTCTCCCACTC
 CAGGGAGCTGTGGTCTATGGTGTGGTGAACATCAGCAACCGCTGTGTGGTTCAGCTCAACTGGAGAGGGTTT
 TCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTCCCGACATCCAAACAAAGGACTGATTTGGGTGGCGCC
 ATTGAATACAGATGGGAGACTGTGGAGTATTATAGACTGTACAACACACTGGATGATTTGCTATTGTATATAA
 ATGCTCGAGAGTTGCCGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAAC
 ATGTACAACACCGGGAATATTGCCAGAGTTAACCTGACCACCAACACGATTGTCTGTGACTCAAACTCTCCCTAA
 TGCTGCCTATAATAACCGCTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG
 GATTTGGGTTATTTATCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAACTCAATGACACCACACTT
 CAGGTGCTAAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCTTCATGGTATGTGGGGTTCT
 GTATGCCACCCGCTACTATGAACACCAAGACAGAAAGAGATTTTACTATTATGACACAAACAGGGAAGAGG
 GCAAACTAGACATTGTAATGCATAAGATGCAGGAAAAGTGCAGAGCATTAACATAACCCCTTTGACCAGAAA
 CTTTATGTCTATAACGATGGTACCTTCTGAATATGATCTTTCTGTCTTGCAGAAGCCCCAGTAAAGCTGTTTA
 GGAGTTAGGGTGAAGAGAAAATGTTTGTGAAAAAATAGTCTTCTCCACTTACTTAGATATCTGCAGGGGTTGT
 CTAAAGATGTGTTTCTTTGCAAGATGTTTGGTGCATAGTTCTACCACACTAGAGATCTAGGACATTTGTCT
 TGATTTGGTGAGTTCTCTTGGGAATCATCTGCCTCTTCAGGCGCATTTTGCAATAAAGTCTCTAGGGTGGGA
 TTGTGAGAGTCTAGGGGCACTGTGGGCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCCTTAAATTA
 GGAATTAAGGAACCTTAAACCTCAGTATGGCGTCTAGGGATCTTTGTACAGGAATATTGCCAATGACTAGTC
 CTCATCCATGTAGCACCCTAATTTCTCCATGCCTGGAAGAAACCTGGGGACTTAGTTAGGTAGATTAATATCT
 GGAGCTCCTCGAGGGACCAATCTCCAACTTTTTCCTCCCTCACTAGCACCTGGAATGATGCTTTGTATGTGG
 CAGATAAGTAAATTTGGCATGCTTATATATTTCTACATCTGTAAAGTGTGAGTTTATGGAGAGAGGCTTTT
 ATGCATTAATTTGTACATGGCAATAAATCCCAAGGATCTGTAGATGAGGCACTGCTTTTCTTTCTCTCTC
 ATTGTCCACCTTACTAAAAGTCAGTAGAATCTTCACTCTATAACTTCCTTCCAAGGCAGCTCAGAAGATTAG
 AACAGACTTACTAACCAATTCCACCCCCACCAACCCCTTCTACTGCTACTTTAAAAAATTAATAGTTTT
 CTATGCACTGATCTAAGATTAGAAAAATTAATTTCTTAAATTTCAATTATGACCTTTTATTTACATGCTCTA
 AGCTATAAGAAATCTGATGGAGCTGCAAAAGTGTAGCATTTATGTTATCTAATAAAGCTCTGGAGCATA
 TGTGCAACTTATGAGTGATCATGTTGTGCATTAATTTTGCCTTTGTTAAGCGTGGAACTTGTAAAGAAAT
 GAAAATTTAAATTTTCTTTCTAGGACGACTATAGAAAAGCTATGAGACTTCAAGTAAATCACTGTCAGTAGT
 TGGAAACCTTGTCTGTATGTGATGTCTTCTGTCTTTTGAATGACTTTATCATCTAGTCTTGTCTATTTT
 TCCTTTGATGTTCAAGTCTAGTCTATAGGATGGCAGTTTAAATGCTTTACTCCCCCTTTTAAAAATAATGAT
 TAAAAATGTGCTTTGAAAAAATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 38

MRPGLSFLALLLFFLGQAAGDLGDIVGPPPIPSPGFSSFPVGDSSSSSFSSSSSRSGSSSSRSLGS
 GGSVSQLFNSFTGSVDDRGTQCQSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
 QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
 LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPTPGSCGH
 GGVDNISKPSVVQLNWRGFSYLYGAWGRDYSPQHFNKGLYWVAPLNTDGRLLLEYRRLNTLD
 DLLLYINARELRITYGQSGTAVYNNNNMYVNMNTGNIRVNLTTNTIAVTQTLPNAAAYNNR
 FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF
 MVCVGLYATRTMNRTEEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG
 YLLNYDLSVLQKPQ

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
 CCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
 GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
 CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCGCCATTGAATACAGATGGGAGACTGTTG
 GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
 GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
 TGTACAACACCGGGNATATTGCCAGAGTTAACCTGACC

$\begin{pmatrix} a_{11} \\ a_{12} \\ a_{13} \\ a_{14} \end{pmatrix}$
 $\begin{pmatrix} b_1 \\ b_2 \\ b_3 \\ b_4 \end{pmatrix}$
 $\begin{pmatrix} c_1 \\ c_2 \\ c_3 \\ c_4 \end{pmatrix}$
 $\begin{pmatrix} d_1 \\ d_2 \\ d_3 \\ d_4 \end{pmatrix}$
 $\begin{pmatrix} e_1 \\ e_2 \\ e_3 \\ e_4 \end{pmatrix}$
 $\begin{pmatrix} f_1 \\ f_2 \\ f_3 \\ f_4 \end{pmatrix}$
 $\begin{pmatrix} g_1 \\ g_2 \\ g_3 \\ g_4 \end{pmatrix}$
 $\begin{pmatrix} h_1 \\ h_2 \\ h_3 \\ h_4 \end{pmatrix}$
 $\begin{pmatrix} i_1 \\ i_2 \\ i_3 \\ i_4 \end{pmatrix}$
 $\begin{pmatrix} j_1 \\ j_2 \\ j_3 \\ j_4 \end{pmatrix}$
 $\begin{pmatrix} k_1 \\ k_2 \\ k_3 \\ k_4 \end{pmatrix}$
 $\begin{pmatrix} l_1 \\ l_2 \\ l_3 \\ l_4 \end{pmatrix}$
 $\begin{pmatrix} m_1 \\ m_2 \\ m_3 \\ m_4 \end{pmatrix}$
 $\begin{pmatrix} n_1 \\ n_2 \\ n_3 \\ n_4 \end{pmatrix}$
 $\begin{pmatrix} o_1 \\ o_2 \\ o_3 \\ o_4 \end{pmatrix}$
 $\begin{pmatrix} p_1 \\ p_2 \\ p_3 \\ p_4 \end{pmatrix}$
 $\begin{pmatrix} q_1 \\ q_2 \\ q_3 \\ q_4 \end{pmatrix}$
 $\begin{pmatrix} r_1 \\ r_2 \\ r_3 \\ r_4 \end{pmatrix}$
 $\begin{pmatrix} s_1 \\ s_2 \\ s_3 \\ s_4 \end{pmatrix}$
 $\begin{pmatrix} t_1 \\ t_2 \\ t_3 \\ t_4 \end{pmatrix}$
 $\begin{pmatrix} u_1 \\ u_2 \\ u_3 \\ u_4 \end{pmatrix}$
 $\begin{pmatrix} v_1 \\ v_2 \\ v_3 \\ v_4 \end{pmatrix}$
 $\begin{pmatrix} w_1 \\ w_2 \\ w_3 \\ w_4 \end{pmatrix}$
 $\begin{pmatrix} x_1 \\ x_2 \\ x_3 \\ x_4 \end{pmatrix}$
 $\begin{pmatrix} y_1 \\ y_2 \\ y_3 \\ y_4 \end{pmatrix}$
 $\begin{pmatrix} z_1 \\ z_2 \\ z_3 \\ z_4 \end{pmatrix}$

FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAGCTGTCTCCATCTTGTCTGTAT
 CCCTGCTCTTGTGTACGTTGTGGAGATGGGGAGCGCTCTGGGGCTGTGCTCCATGGCGAGCT
 GGATACCATGTTTGTGTGGAAGTGCCCGGTGTTTGCATGCCGATGCTGTCCATGTGGAAAC
 AACTCCACTGTAACTAGATTGATCTATGCACCTTTTCTTGTCTGTGTGGAGATTGTGTAGCTTG
 TGTAAATTTGTGATACAGGAATGGAAGAACAACTGAATAAGATTCCGTGGATTTTGTGAGAATG
 AGAAAGAGTGTGTGCCCTTGTAAACATTTTGGTTGGCTATAAAGCTGTATATTCGTTTGTGCTTT
 GGTTTGGCTATGTTCTATCTTCTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAATGA
 TCCTAGAGCTGCAGTGCACAAATGGATTTTGGTCTCTTAAATTTGCTGCAGCAATTGCATTA
 TTATTTGGGGCATCTTTCATTTCCAGAAGGAACTTTTACAACCTGTGTGTTTATGTAGGCATG
 GCAGGTGCCCTTTTGTTCATCCCTACACAACCTAGTCTTACTTATTGATTTTGCACATTCATG
 GAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGAACCTCGAGATGTTGGTATGCAGCCTTGT
 TATCAGCTACAGCTCTGAATTAATCTGCTGTCTTTAGTTGCTATCGTCTGTCTTTGTCTAC
 TACACTCATCCAGCCAGTTGTTTCCAGAAAACAGGCGTTCATCAGTGTCAACATGCTCCTCTG
 CGTTGGTGCTTCTGTAATGTCTATACTGCCAAAAATCCAAGAAATCAACAACAGATCTGGTT
 TGTACAGTCTTCAGTAATTACAGTCTACACAATGATTTGACATGGTCAGCTATGACCAAT
 GAACCAAGAAACAAATTTGCAACCCAAGTCTACTAAGCATAATTTGGGTACAATACAACAAGCAC
 TGTCCCAAAGGAAGGCGAGTCACTCCAGTGTGGCATGCTCAAGGAATTTATAGGACTAATTC
 TCTTTTGTGTGTGTATTTTATCCAGCATCCGTACTTCAAACAATGTCAGGTTATATAAA
 CTGACTCTAAACAAGTGAATCTACATTAATAGAAGATGGTGGAGCTAGAAGTATGGATG
 ACTGGAGGATGGGAGCAGTGTTCACCGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACA
 GTTATTCCTTCTTCCAGTCTGTCTTCTGCTTCACTTTATATCAATGACCTTACC
 AACTGGTCCAGGATGAACCCCTCTCGTGAGATGAAAGTCACTGGACAGCTGTCTGGGTGAA
 AATCTCTTCCAGTTGGATGGCATCGTGTGATGTTTGGACACTCGTGGCACCACTTGTTC
 TTACAAATCGTGTATTTGACTGAGAGCTTCTAGCATGAAAGTCCCACCTTTGATATTATGC
 TTATTTGAAAACAGTATTTCCCAACTTTTGAAGTTGTGATGTTTGTCTCCCATGTAAAC
 TTCTCCAGTGTCTGGCATGAATTAGATTTTACCTGCTGTCTATTTTGTATTTTCTTACCAA
 GTGCATTGATATGTGAAGTAGAATGAATTTGCAGAGGAAAGTTTATGAATATGGTGATGAGT
 TAGTAAAAAGTGCCCATTTATTTGGGCTTATTCCTGCTCTATAGTTGTGAAATGAAGAGTAAAA
 ACAAAATTTGTTTGACTATTTTAAAAATTAATTAGACCTTAAGCTGTTTATGACCAATTAAA
 GCAAAATGATGGCTGCCCTTTTGAATATTTGATGTGTTGGCCTGGCAGGATACTGCAAAAGAAC
 ATGGTTTATTTTAAAAATTTATAAACAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA
 AGGTTTACCCTTGATACGGAATTTACACAGGTAGGGAGTGTTAGTGGACAATAGTGTAGG
 TTATGGATGGAGGTGTCGTACTAAATGAATAACGAGTAAATAATCTTACTTGGGTAGAGA
 TGGCCTTTGCCCAACAAGTGAACCTGTTTGGTGTGTTTAACTCATGAAGTATGGGTTCAGT
 GGAATTTTGGAACTCTGAAGGATTTAGACAAGGTTTGAAGGATAATCATGGGTAGAGA
 AGGAAGTGTTTGAAAGTCACTTTGAAAGTGTAGTTTGGGCCAGCACGGTAGCTCACCCCT
 GGAATCCCCAGCATTGGGAGCTTAAAGTGGGTAGATTACTTGAGCCCAGGAATTCAGACCA
 GCTTGGCACAATGGTGAACCTGTTCTATAAAAAATAATCTGGCTTTGAGCATATGCTCTGGGT
 CAGCATGAGAGGCTAGTGAAGATTGCTGAGCCAGAGCCAAAGGTTGCAAGTGAAGCAAGTCA
 CGTCACTGCATCTAGCTGGCAGAGTAAAGCCAAAAAATATATATATTGAAATCAAGG
 AGGCAAAATTTGACAGGAAGGAAGTAACTGCAAAACCACTAGGCTTTAGTAGGTACTTAT
 ATAAAACTAGTCCAGTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATA
 GCTCAGATAGCTAATTAGGAATTTCAAGTTGGCCATAAATAGCATCTCTCTGCATTTAA
 AAATAATTTCTATTCAAATACATGCATATTGATTTACACCTCATAGCTGTGATAATTATGT
 GATGTGGATTGCTGTGTCCAGCATGACCCATAAACAGGTCAAGAAATGATGGAATGTTTT
 AGAATAAACTCCTGCTTATAGTATACACAGTTCAAAGATGTTTAAATGCTTTTGTAT
 TTACTGCCATGTAATTTGAATATATAGATTATTGTAACCTTCAACCTGAAAACTCAGCAGT
 ATGAGAGTTTGTGTTATTTGTATGTGCTACTAGTGTCTAATGAAGCTTTTAAATCTACAAAT
 TCTTTCTTAAAAATTTTAAATGTGAATGGAATATAACATCTAGCTTAAATCCCCAAC
 TTATCTGTGTGTAGACATTGTATCCACAATTTTGAATGGCTGTGTTTACCCTCTAAATAA
 ATGAATTCAGAGAAAAA

FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVVPCNILVGKAVYRLCFGLAMFYLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILQLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMyltWSAMTNEPETNCNPSSLIIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVITYSYFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSSWIGI
VLYVWTLVAPLVLTNRDFD

GCAGAGAAAGAAGCTGCTCCATCTTGTCTGTATCCCGCTGCTTCTTNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGCGTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAAGTGCC
CCGTGTTTGTCTATGCCGATGCTGTCTAGTGGAAACAANTCCACTGTAACTAGATTGATCTA
TGCACTTTTCTTGCTTGTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACACGGAATGGAAG
AACAACTGAATAAGATTCTGGATTTTGTGAGAAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATACGTTTGAGCTTTTGCTTTGGCTATGCTTCTATCTTCTTCT
CTCTTTACTAATGATCAAGGTGAAGTAGCTAGCTGCTTAGAGTGCAGTGCACAATGGAT
TTTGGTCTCTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGTCTNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNATGCCGATGCTGTCCTAGTGGAACAANTCC
ACTGTAATTAGATTGATNTATGCACCTTTNTTGTCTTGTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTAAATTGCTGCAGCAATTGCAATTATTATTG
GGGC

FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCTAGTGGAAACAACCTCCACTGTAAGTATGATCTATGCACTT
TTCTTGCTTGTGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTGTCCCTTGTAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTGTAACCTGGATTGATCTATGCACCTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA
AGATTCCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCCCTGTAACATTTTGGTTGGC
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTATGGGGCATTCCTTCATTCCAGAAGGAACTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAAGTAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTTGAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCCGTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC
GTTTCATCAGTGCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

FIGURE 46

CTCGGGCGCGCAGGCGAGCTCGGTTTGCCCTGCGATTGAGCTGCGGGTCGCGGCCGGCGCGGCTCTCCAAT
 GGCAAATGTGTGTGGCTGGAGGCGAGCGGAGGCTTTCGGCAAGGCGAGTCGAGTGTATTGCAGACCGGGCGGAG
 TCCTGTGAAAGCAGATTAAGAGAAACATTTATTAACGTGTCAATTACGAGGGAGCGCCGCGCGGCTGTGCG
 ACTCCCCGCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAGAGAAAGCGGAAAGAGGCGAGATTAC
 GTCGTTTCAGCCCAAGTCGACCTGATCGATGGCCCTCTGATTTTATCAGGATATTGATTTATAGCGATTGCC
 CCTGGTTTGTGTGTAGCAGCACACACAGCTGCACACAGGCTCTGGCTCGCTTCCTCCCTCGTTTCAGGCTCC
 TGGGCGAATCCCCATCTGTTTCACTCTCCGCGAGGGCGAGGAGCGAGAGTGTGTGCAATTGCGAGTGTG
 AAGAGGGACGAGGAAAGAAACAAAGCCACAGAGCGCACTTGAGACTCCCGCATGCCAAAAGAGACACAGAT
 CAGCAAAAAAAGAAATGCGGCCCGCGAGCCTCGTGCTGTGCTGTCTCCGCAACTGTGTTCTCCCTCTGTGG
 TGGAGCTCGGCTTCTGTGCGACACCGCTGAAAGGCGAGTTTCAGAGGGACCGCAGGAAACATCCGCCCA
 ACATCATCTGTGTGACGCGAGCAGCAGGATGTGGAGCTGGGTTCCATCGAGGTGATGAACAGACCCGCGCG
 ATCATGGAGCAGGGCGGGCGCACTTCATCAACGCCTCTGTGACCAACCCATGTGCTGCCCTCACGCTCTC
 CATCTCACTGGCAAGTACGTCCAACACACACACTTACCAACAATGAGAATGCTCCTCGCCCTCTGTGG
 AGGCACGACGAGAGCCGACCTTTGCGGTGTACTCAATAGCACTGGTACCGGACAGCTTTCTTGGGAAG
 TATCTTAATGAATACAACGGCTCTACGTGCCACCCGGCTGGAAGGAGTGGTCCGACTCTTAAAACTCCCG
 CTTTATAACTACACGCTGTGTGCGAACGGGTGAAAGAGAGAGCAGGCTCCGACTACTCCAAGGATTACCTCA
 CAGACCTCATCAACATGACAGCGTGAGCTCTTCGCGACGTCCAAGAAGATGTACCCGACAGCGCGAGTCTC
 ATGGTCAATCAGGCAATGAGCCCCCAGCGGCTGAGGATTACGCCCCAATATTACGCGCTCTTCCAAACGC
 ATTCAGGCAATCAGCGGAGCTACAATACGCGCCCAACCCGGACAAACATGGATCATGGCTACACGGGGC
 CCATGAAGCCCATCAACATGAATTCACCAACATGCTCCAGCGGAGCGGCTTCGAGACCTCATGTCGGTGGAC
 GACTCCATGAGACGATTTACAACATGCTGGTTGAGACGGGCGAGCTGGACAAACAGTACATCGTATACACCCG
 CCGACAGGTTTACCACATCGGCGAGTTTGGCTGGTGAAGAGGAATCCATGCCATATGAGTTTACATCAGGG
 TCCCGTTCTACGTGAGGGGCCCAACGTTGGAAGCGGCTGTCTGAATCCCCACATGTCCTCAACATTGACCTG
 GCCCCACCATCTGACGATGTCGAGGCTGGACATACCTCGGATATGGACGGAAATCCATCTCTCAAGCTGCT
 GGACAGCGGAGCGCGGTGAATCGGTTCACTTGAAAAGAGAGATGAGGCTGTGCGGGACTCTCTTCTGTGTG
 AGAGAGGCAAGCTGCTACACAGAGAGACAATGACAGGTGGAGCGCCAGGAGGAACCTTCTGCCAAGTAC
 CAGCGTGTGAAGACCTGTGTGACGCTGCTGAGTACAGACGCGGCTGTGAGCAGCTGGGACAGAGCTGGCAGT
 TGTGGAGGACGCCACGGGGAAGCTGAAGCTGCATAGTGAAGGCGCCCATGCGGCTGGCGGCACTACGAGCGCC
 TCTCAACCTCTGCTGCCAAGTACTACGGGCGAGGCGAGGCGCTGCACCTGTGACGCGGGGACTACAAGCTC
 AGGCTGGCCGCGAGCCGGAANAACCTTCAAGAAGAATACAAGGCGCACTATGTCCGCACTCGCTCCATCCG
 CTCATGGCCATCGAGGTGGAACGGCAGGCTGACACGCTAGGCGTGGGTGATGCCGCCAGCGCCGAAACCTCA
 CCAAGCGCACTGGCCAGGGGCCCTTAGGACCAAGATGACAAGGATGTTGGGACTTCAGTGGCATCGGAGGCG
 CTTCCGACTCATCAGCGGCCCAACCCATTAAAGTGACACATCGTGTCACTCTAGAGGACGACAGATTTGA
 GTGTGACCTGACCTGTACAAAGTCCCTGAGGCTGGGAAGTCCGAGGTCACTGAGGAAAGCGGCCGACAGATTTGAC
 CCTCGCAACAAAATTAAGAACTGAGGAGCGCACAAAGGCGCGCTCAAGCACAGAGGCTCCAGTCTGCATCTTTCAG
 TGTCAAAATTCAGTACCAACGAGCGCACAAAGGCGCGCTCAAGCACAGAGGCTCCAGTCTGCATCTTTCAG
 GAGGGCTGCAAGAGAGGACCAAGGTGTGGCTGTTGCGGGAGCAGAGCGCAAGAGAAACTCCGAAAGCTGC
 TCAAGCGCTCGAGAACACAGCACTGTGAGCTGCGAGGCTCACTGCTTCCACCCAGCACAAACGAGTGTGAG
 CAGCGCGGCTTTCGAGCACTGGGCGCTTCTGTGCTGACCAAGCGCACAAATAACACGATCACTGTCGATGAT
 GAGGACCATCAATGAGACTCACAATTTCTCTTGTGAATTTGCAACTGGCTTCTAGAGTACTTTGATCTCA
 ACACAGGCCCTACCGCTGATGAATGAGTGAACACTGSAAGGATGTCTCAACAGCTACAGCTCAG
 CTCATGGAGCTGAGGAGCTGCAAGGTTTCAAGAGCTGTAAACCCCGGACTCGAAACATGGACCTGGATGGAG
 AAGCTATGAGCAATACAGGCGATTTGAGCTCGAAAGTGGCCAGAAATGAAGAGACCTTCTTCCAAATCACTGG
 GACAACTGTGGGAGGCTGGGAAGTTTAAAGAAACACAGAGGTGACCTCCAAAAACATAGAGGCACTCACTGA
 TCTCAGGCAATGAAAAACCATGTGGGTGATTCCACAGCTGCTGCTATTGGCCAGGAGGCTGAGAAAGC
 AAGCAGCAGCTCTCAGTCAACATGACAGATTTCTGGAGGATAACAGCAGGACGAGATATCTCAGGAAGTCC
 ATTTTTCGCCCTGCTTTGCTTTGGATTTATACCTACCGAGTGCACAAATGCAATTTTCTGATCAAAAGTCC
 ACCATCAACCTCCCCAGAGCTCACAAAGGAAACGGAGAGAGCGAGGAGAGAGATTTCTTGAAATTTTC
 TCCAAAGGCGAAAGTCAATTTGAAATTTTAAATCATAGGGGAAAGAGCTGCTGTTTCTAAATCTTATCTT
 TTGTTTGTGACAAAGAAGGAACATAAGAGCAGGACAGAGGCAACGTGTGAGAGGCTGAAACAGCTGACGAGG
 TTTGCAATGAGTCAGTAGCAAAAGAGATGACATTTACCTAGCACTATAAACCTGTGGTTCCTTGAGGAA
 CTGCCCTCATTTGATATATGTGACTATTTACATGTAATCAACATGGGAACCTTTTGGGGAACCTAATAGAAAT
 CCCAATTTTCAGGAGTGGTGTGTAATAACGCTCTGTGCCAGTGTAAAAA

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDDQDVELGSMQ
 VMNKTRRIMEQGGAHFINAFVTPMCCPSRSSILTGKYVHNHNTYNNENCSSPSWQAQHE
 RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWGLLKNSRFYNYTLCRNGVKEKHGSD
 YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFNPASQHITP
 SYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
 YIVYTADHGYHIGQFGLVGKGSMPYEFDIRVPFYVRGPVNEAGCLNPHIVLNIDLAPTILDI
 AGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
 FLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLLHKCKGPMRLGGSRALSNLVPKY
 YGQGEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAQ
 PRNLTKRHWPAPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDDLKYKS
 LQAWKDHKLHIDHETIETLQNKIKNLREVRGHLKKKRPEECDCHKISYHTQHKGRLKHRGSSL
 HPFRKGLQEKDKVWLLREQKRKKLRLKLLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
 PFCACTSANNTYWC MRTINETHNFLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
 HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
 GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC
 TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCCCTGCTGCTGCTGCTGCTGCTGGCCACC
 TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
 CCGAGTCCGCCGGGCCAGCCTTGGCCCTTCCGGCGGCGGGCCACCTGGGAATCTTTCACC
 ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC
 CCCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCACCAGCCACCATCCCCGCCA
 CGCTCGCTGAGGCTGCTGTGCGCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG
 TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
 GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGACTATGGC
 AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGTGAAGGTTTGGGGAGTGGAGAGCAAGG
 GTGCTCTTTGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCCAGTGAGCCCCAGAAATG
 ACAAGCGTGCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
 ATCAGGCTGCTGCAGGCCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCTTTT
 GGTTTGAGAAGGCAGTGTGAGGCTGCACAGTCAATTATCGGTGCCTTAGTCCAAGAAAAT
 AAAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 49

MLGLLGSTALVGWITGAAVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRRAPWPFR
 RRGHLGIFHHHRHPGHVSHVVPNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

$\frac{p^{(1)}(t)}{q^{(1)}(t)}$
 $\frac{p^{(2)}(t)}{q^{(2)}(t)}$
 $\frac{p^{(3)}(t)}{q^{(3)}(t)}$
 $\frac{p^{(4)}(t)}{q^{(4)}(t)}$
 $\frac{p^{(5)}(t)}{q^{(5)}(t)}$
 $\frac{p^{(6)}(t)}{q^{(6)}(t)}$
 $\frac{p^{(7)}(t)}{q^{(7)}(t)}$
 $\frac{p^{(8)}(t)}{q^{(8)}(t)}$
 $\frac{p^{(9)}(t)}{q^{(9)}(t)}$
 $\frac{p^{(10)}(t)}{q^{(10)}(t)}$
 $\frac{p^{(11)}(t)}{q^{(11)}(t)}$
 $\frac{p^{(12)}(t)}{q^{(12)}(t)}$
 $\frac{p^{(13)}(t)}{q^{(13)}(t)}$
 $\frac{p^{(14)}(t)}{q^{(14)}(t)}$
 $\frac{p^{(15)}(t)}{q^{(15)}(t)}$
 $\frac{p^{(16)}(t)}{q^{(16)}(t)}$
 $\frac{p^{(17)}(t)}{q^{(17)}(t)}$
 $\frac{p^{(18)}(t)}{q^{(18)}(t)}$
 $\frac{p^{(19)}(t)}{q^{(19)}(t)}$
 $\frac{p^{(20)}(t)}{q^{(20)}(t)}$

FIGURE 50

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA
CTACTGGGCCTGATTGGGGGCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
GTACTCAGGGCTACTGGCTGGGTGGAAGTGAGTGCTGGGTACCCCCATCCGCAACGTCA
CTGTGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCTACTGAGAGC
TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
CATGTGGTGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG
TGTCCATCCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCATCCTCGGCTGG
AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTAT
GTGCCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGCTTGTGGAGGCCATTGACACCCA
GGTGGATGGCAGAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAGTGAGCC
CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTACCTGGGGCAGCAGCCCTGGCTGGGAT
GACGGTGACACCCGCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
GGAGCTGGACTTGGAGGGCAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGC
CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAG**TAA**CCC
ATGGCCTGCACCTCCTGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCT
CCAGCCCTCTTCTCCTTCTCTGGGGAGGAGGGGTTCTTGAGGGACCTGACTTCCCCTGC
TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCA
GGGACTATTTTCTGCACACGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC
ACAGTGAGGACTTCCAGGACCCAGAATAAGCCAATGATTTACTTGTTCACCTGGAAAAAAA
AAAAA

FIGURE 51

MSDLLLLGLIGGLTLLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKRCRAVGSILSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRRVHPALDITYIKERKLCAYPRLEIYQEDQIHFMCLAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSVSVSLEVSPGSRETSAAATLSPGAS
SRGWDDGDRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

FIGURE 52

CCGCGGGAACGCTGTCTCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCT
 GCGCGCGCCAGT**CATG**ACCCCTGCGCCCCCTACTCCTCCCGCTCCATCTGCTGCTGCTGCT
 GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
 CCTCCAAGTGGAGACCTGTGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGA
 GACACGCTTCACATACACTACACGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
 GACCAGAGACCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
 GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTGGCCTAT
 GGAAAACGGGGATTTCACCACATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
 GATTGCACTAATCCGAGCCAACCTACTGGCTAAAGCTGGTGAAGGGCATTTCCTCTGGTAG
 GGATGGCCATGGTGCCAGCCCTCCTGGGCTCATTTGGGTATCACCTATACAGAAAGGCCAAT
 AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAA**TA**
ATAAATAATAAATTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF
PPSPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNKSKKK

FIGURE 54

CCCGGGAACGTGTTCTCTGGCTGCCGCACCCGAACAGCCTGTCCTGGTGCCCGGGCTCCCTGC
CCCGCGCCCACTCATGACCCCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGAGAGCCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACATAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAGGG
ATGGCCATGGTGCCACCCTCCTGGGCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
ATAATAAAATTTTAAAAAACTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGTTTATAGAAGCTTGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGAAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAATAAATTTTAAAAAACTTAAAA

FIGURE 56

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAAATCGGGGGAG
 TGAGGCGGGCCGGCGCGCGACACGGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAAAATGTTCTGGATTTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCT
 GTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGG
 TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTG
 CTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
 TTCCACAGCACAACAGCCCTGCATGGGTTTGTGTTTTTTTACTGCTCACTCCCAACCTT
 TTGTAATGCCATTTTCTAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
 AAAATCACGAGAACACCTAAACAACAACCAAAAATCTATTGTGGTATGCACTTGATTAAGTT
 ATAAAAATGTTAGAGGAACTTTCACATGAATAATTTTGTCAAATTTTATCATGGTATAATT
 TGTA AAAATAAAAAGAAATTA CAAAAGAAATATG GATTTGTCAATGTAAGTATTTGT CATA
 TCTGAGGTCCAAAACCAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTC AAATGTGGT
 CTCTTCTGTGTC AAATGTTAAATGAAATATAAACATTTTTT AGTTTTTAAATATTTCCGTGG
 TCAAAATTTCTCTCACTATAATTGGTATTTACTTTTACCAAAAATCTGTGAACATGTAAT
 GTAAC TGGCTTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
 GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGTCTTCCGCTGTGCCTCTCATT
 CCAAGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
 CACATCCACCAC TG

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDA AVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

FIGURE 58

TTCTTGGCTAAAAATCGGGGGAGTGAGGCGGGCCGGCGCGCGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCATTTGGCTTTTCGTGGTTTCATGTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTGGC

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC
 TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
 GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC
 ATGCCTGTGGTGTATTAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
 GTCCGAGGTGATAGTTACAGTGAAGGTGTTTGGSTCAAACAGGTGCTCGCATTGGCTTTT
 CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT
 ATGTTGCTAAAGAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC
 ATCTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT
 TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
 CCATTGCTGCTGGTGACTATTTTTTACAGGGTGGTGATTATCATAGATGCAGCTGTTATT
 TATCCCACCATGAAAGATTNAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGC
 CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
 GTTTGGGTCAAACAGGTGNTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
 CTGATTGNATTCTATGCGGATTCTTCTTGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
 ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC
TTCCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

FIGURE 62

GGGAGGCTGTGNCCGTTTTGTTTTNTTGGCTAAAATCGGGGGAGTGAGGCGGCCCGGCGCGG
 CGNGACACCGGGTCCGGGAACCATTGCACGACGGGGTGGACTGACCTGAAAAAATGTTTG
 GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATT
 GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
 TATTTATCCCACCATGAAAGATTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCA
 TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
 GGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
 ATNTCTGATTGCATCTATGTGGATTCTTTTTGGAGTTATGTTGCTAAAGAAAAAGACATAG
 TATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATNTTTTTTGAGGGGCTG

FIGURE 63

CGACGCCGCGCTG**ATG**TGGCTTCGCTGGTGTGCTCTGGCTGTGCTGCTGCTGGCCGTCC
TCTGCAAGTTTACTTTGGGACTATTCTTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC
AAACGGCCCCAGCCGCCCTGGTAACGTGACAAGAGGGCAGGAAGAGGTTCTCTAAACAAAGC
TTTTTTCAGCCAAACCAAGTCCGGGAGAAAGCTGGATGTGGTGGTAAATTTGGCAGTGGCTTTGGGG
GCCTGGCTGCAGTGCATTTCTAGCTAAAGCTGGCAAGCGAGTCTGGTGTCTGGAACAAACAT
ACCAAGGCGAGGGGGTCTGTGTCATACCTTTGGAAAGAAATGGCTTGAATTTGACACAGGAAT
CCATTACATTTGGGCTGTGGAAGAGGGCAGCATTTGGCCGCTTTATCTTGGACAGATCACTG
AAGGGCAGCTGGACTGGGCTCCCTCTCTCTCTTTGACATCATGGTACTGGAAGGGGCCC
AATGGCCGAAAGAGTACCCCATGTACAGTGGAGAGAAGCCTACATTAGGGGCTCAAGGA
GAAGTTTCCACAGGAGGAAGCTATCATTTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCCA
GTGGAGCCCCCTCATGCCATCTCTGTTGAAATTCCTCCCATTTGCCCGTGGTTCAGCTCCTCGAC
AGGTGTGGGCTGTGACTCGTTTCTCTCCATTCTCTCAAGCATCCACCCAGAGCTGGTGTGA
GGTCTGACAGCAGCTGGGGGCTCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCGCA
CTTACGGTGTCAACCCCAACCACAGTGCCTTTTCCATGCACGCCCTGTCTGGTCAACCACTAC
ATGAAAGGAGGCTTTTATCCCGAGGGGGTTCAGTGAATTCCTTCCACACCATCCCTGT
GATTACAGCGGGCTGGGGGCGCTGTCTCTCAAAAGGCCACTGTGCAGAGTGTGTTGCTGGACT
CAGCTGGGAAAGCCTGTGGTGTGACGTGTGAAGAAGGGCATGAGCTGGTGAACATCTATTGC
CCCATCGTGGTCTTCAACAGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGGAACGC
CCGCTGCTGCCAGGTGTGAAGCAGCAACTGGGGAGCGTGCGGCCCGGCTTAGGCATGACCT
CTGTTTTCATCTGCTGCTGCGAGGCACCAAGGAAGACCTGCATCTGCCGCTCCACCACTACTAT
GTTTACTATGACACGGACATGGACCAGGCGATGGAGGCTACGCTCTCCATGCCACAGGGAAGA
GGCTGCCGAACACATCCCTCTTCTCTTCTCTGCTTTCCCATCAGCCAAAGATACCGAGCTGGG
AGGACCGATTCCACGGCCGCTCCACCATGATCATGCTACATCCCACTGCTGAGTGGTGT
GAGGAGTGGCAGGCGGAGCTGAAGGGAAAGCGGGGCGAGTGAATGAGACCTTCAGAAACTC
CTTTGTGGAAGCCTCTATGTCAGTGGTCTTGAATCTTCCACAGCTGGAGGGGAAGGTGG
AGAGTGTGACTGCAGGATCCCCACTCACCACCAAGTCTATCTGGCTGCTCCCGAGGTGCC
TGCTACGGGGGTGACCATGACCTGGGCCGCTGCACCTTGTGTGATGGCTCCTTGAGGGC
CCAGAGCCCCATCCCCAACCTCTATCTGACAGGCGAGGATATCTTCACTGTGGACTGGTGC
GGGCCCCGCAAGGTGCCCTGCTGTGCAGCAGCGCCATCTGAAGCGGAACCTGTACTCAGC
CTTAAGAATCTTGATCTAGGATCCGGGCAAGAGAAAGAAAT**TAG**TTCCATCAGGGAGG
AGTCAGAGGAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGCTCTTTCTG
CATTAGTTCCTTGACGATAAAGCACTCTAATTTGGTTCTGATGCTGAAGAGAGGCCCTAG
TTTAAATCACAATCCGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA
TCTTTAGCCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTTGATG
TCTCATGACGAGCGGCGCTCTGCTATCCCTCACCATGCTCTCTAATCAGTGAATCAAGCGA
ATATTCATCTGTGGATAGAACCCCTGGCAGTGTGTGACGTCAACCTGGTGGGTTCAGTTT
TGTCTTGAGGCTTCTGCTCTCATTCATTTAGTGTACGCTGCACAGTTCTACACTGTCAAGG
GAAAAGGGGAGACTAATGAGGCTTAACTCAAACCTGGGCGTGGTGTGTTGGTTCGCAATTCATA
GGTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGGTTCTAGTGGCTCTTCAGGGGACAGGAAT
GCCTGTGTCTGGCCAGTGTGGTCTGGAGTCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA
GGGTGCATGTGCATGATCATATCCAATTCATATGGAAGTCCCGGCTCTGCTCTTCTATCA
TCGGGGTGGCAGCTGGTCTCAATGTGCCAGCAGGAGCTAGTACCTGAGCCTCAATCAAGC
CTTATCCACCAAAATACACAGGGAAGGGTGATGCAGGGAAGGAGTCACTCAGGAGTCAGGGA
TGGACTGGTAAGATGAATCTTTGCTGGGCTGAAGCAGGCTGCAGGGCATTCAGCCCAAGGG
CACAGCAGGGGACAGTGCAGGGAGGTGTGGGGTAAGGGAGGGAAGTCACTCAGAAAGGGA
AAGCCACGGAATGTGTGTGAAGCCAGAAATGGCATTTGCAAGTTAATAGCATGTGAGGG
TTAGACAGGTAGGTGAATGCAAGCTCAAGGTTTGGAAAAATGACTTTTGCATGATGCTTTG
GTATCAGACATACGAAAGGTCTCTTTGTAGTTCGTGTTAATGTAACATTAATAAATTTATTG
ATTCATTGCTTTAAAAAAAAAAAAAAAA

FIGURE 64

MWLPLVLLLVALLLAVLCKVYLGLFSGSSPNPFSEDKRPPAPLVTDKKARKKVLKQAFSAN
 QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
 RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
 EEAIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
 LGASSELQAVLSYIFPTYGVTPNHSAFMSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA
 GGAVLTKATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAGLFNTYEHLLPGNARCLP
 GVKQQLGTVRPGLGMTSVFICLRGTEKEDLHLPSTNYYVYDMDQAMERYVSMFREEAAEH
 IPLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEWQAEKKGKRGSDYETFKNSFVEA
 SMSVVLKLFPPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRHLPCVMASLRAQSPI
 PNLylTGQDIFTcGLVGALQgALLcSSAILKRnLYSDLKNLDSRIrAQKKKN

[illegible]

FIGURE 66

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLD
 SESESELESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEPPKKVRKPALTAIEGTAHG
 EPCHFPPFLFDKEYDECTSDGREDDGRLWCATTYDYKADEKWGFCETEEEAARRQMGEAEMM
 YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMFEX
 LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLIAMVVLVSRL

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FIGURE 67

CTTCCCAGCCCTGTGCCCCAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCC**ATG**GCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCTTGCCCCAGCTGGATGCAC TGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTACCATCAGGGACTACGGTGTGTCTTGG
TACCAGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAATGCCT
GTGTCCTACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCC**TAG**GGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCT
GCCCCTGACCTTGGGTCCCTTTTAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

FIGURE 69

GCGGCCCGCCCGGAGACGGGGCCGGGGGCGCGGGCGGCGGATGCGGCGCCCGGGGCGG
 CGATGACCGCGGAGCGGCACGCCGCGGGGCCCGGCCCTGACCCCGCGCGCGCGCGCTGAGCCCC
 CCGCGCGAGGTTCCGACAGGCCGAGATGACGCCCGAGCCCTGTTGCTGCTCCCTGCTGCCG
 CGCTGCTGCTGGGGGCTCTCCACCAGCGCGCGCGCGCGCGGAGGCCCCCAAAGATGGCGGAC
 AAGTGGTCCACAGGCGAGTGGCCCGCTGGGCGCACTGTGCGCGTGCAGTGGCCAGTGGGA
 GGGGAGCCCGCGCGCTGACCATGTGGACCAAGGATGGCCGACCATGCACAGCGGCTGGGA
 GCGCGCTCCGCGTGTGGCCGAGGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCGCGG
 GTGTACGTGTGCAAGGCCACCAACGGCTTCGCGAGCCTGAGCGTCAACTACACCTCGTCTGT
 GCTGGATGACATTAGCCACAGGAGGAGCGCTGGGCGCGCAGCTCTCTGGGGGTCAAG
 AGGACCCCGCCAGCCAGCACTGGCCAGCAGCGGCTTCCACAGCCCTCCAAGATGAGGCGG
 CGGCTGATCGCACGGCCCTGGGCTAGCTCCGTGCGGCTCAAGTGGGTGGCCAGCGGGCACCC
 TCGGCGCGACATCAGTGGATGAAGGACGACAGCGCTTGAAGCGCCACAGGCGCGCTGAGC
 CCAGGAAGAAGAAGTGGACACTGAGCCTGAAGACCTCGGCGCGGAGGACAGCGGCATATAC
 ACCTGCGCGGCTGTGCAACCGCGCGGGGCGCATCAACGCGCTACAGGCTGGATGTGATCCA
 CGGAGACCGCTTCCAAGCGGTGCTCACAGCACGACCGCGTGAACACAGCGGTGAGTCTCG
 GGGGAGCCAGCTCTTCCAGTCAAGGTGGCGCAGCGACCGTGAAGCGGTGATCCAGTGGCTG
 AAGCGCGTGGAGTACGGCGCGGAGGGCGCCACACCTCCACATCGATGTGGGCGGCGAGAA
 GTTGTGTGCTGTGCCACCGGTTGACGTGTGGTTCGCGCGCGCGCGCTTCTACCTCAATAAGC
 TGCTCATACCCGTCGCCCGCAGGACGATGCGGGGATGTACATCTGCTTGGGCGCACAGC
 ATGGGCTACAGCTTCGCGAGCGCTTCTCTACCTGCTGCCAGACCCAAACCGCGCGAGGCG
 ACCTGTGGCCTCTCTGCTCTCGGCCACTAGCTTCGCTGGCGGCTGTCTATCGGCACCCAG
 CCGGCGCTGTCTTATCCTCTGGGCACTGCTCTGTGGCTTTCGAGCGCCACGAAGAAGCGG
 TGCACCCCGCGCTTCCCTCTCCCTGCTGGGACGCGCGCGCGGAGCGCGCGCACCG
 CAGCGGAGACAAAGACCTTCCCTCGTTGGCGCGCTCAGCGCTGGCCCTGGTGTGGGCTGT
 GTAGGAGACATGGGCTCTCGGCGAGCCCCACGACTTACTGGGCGCAGGCGAGTTGCTGGC
 CCTAAGTGTATCCCAAACCTCTACACAGACATCCACACACACACACACACTCTCACAC
 ACATCACACGTTGGAGGAGGTCACACGACATCCACTTCACTGTGCTAGACGCGACCCGT
 ATCTGCAGTGGGACGCGGGGGCGCGCGCAGACAGGACAGTGGGAGGATGAGGACGAGGCT
 GCAGACGAAGCGAGGAGCCATGGCGAGGAGGATGGCGACACAGCCAGGACGCTCTGTGTG
 TGAGGCTAGGCCCCGGACACACACACACACACACACTTGGATGCAATGATGCAC
 ACACATGCGCGCACAGATGCTCTCTGAAGGCACACGTCACACACGACATGCACAGATATG
 CCGCTGGGACACAGATAGCTGCCCAAATGCACGACACGACACAGACATGCCAAGACA
 TACAAGGACATGCTGCTGAACATACACACGACACACCCATGCCAGATGTGCTGCTGGACA
 CACACACACACACAGGATATGCTGTCTGGACGACACACGTCAGATATGGTATCCGGACACA
 CAGTGCACAGATATGCTGCTGGACACACAGATAATGCTGTGACACACATGACACAGG
 ATATGCTGCTGGACACACACACACACACACGCTGCACAGATATGCTGTCTGGACACGACAC
 ACATGACAGATATGCTGCTGGACACACACTTCCAGACACAGTGCACACGCGAGATATGCTG
 GCCTGGACACAGCAGATATGCTGTCTAGTACACACACAGCAGACATGCTGTCCGGAACAC
 ACACACGATGCACAGATATGCTGTCTGGACACACACACGACGACGAGATATGCTGCTGGAC
 ACACACACAGATAATGCTGCTCAACACTCACACAGTGCAGATATGCTGCTGGACACACACA
 TGTGTCCGATATGCTGTGGACATGCACACAGTGCAGATATGCTGTCCGATACACAGC
 CAGCAGACATGACAGATATGCTGCTGGGACACACTTCCGACACACATGACACACAGGT
 GCAGATATGCTGCTGGACACACACAGATAATGCTGCTCAACACTCACACAGTGCAGATA
 TATTGCTGGACACACATATGTCAGATATGCTGTCTGGACATGCACACAGTGCAGATA
 TGTGTCCGATATGCTGTGGACATGCACACAGTGCAGATATGCTGCTGGGACACACTTCCGGA
 CACACATGCACACAGGTCAGATATGCTGCTGGACACACGACAGACTGACGTGCTTTTGG
 GAGGGTGTGCGGTGACGTCAGTACGTGTGCGGTGAGGCTGACAGTGTGATGAGGGACTTT
 CCTGCTCCACGCTCACTCCCCAACCTCTGCGCGGCTCTGTCCCCGCTCAGTCCCCGCTC
 CATCCCCGCTGTGCTGCTGCTGCTGCTGGCGGCTATTTTGGACACTGCTTGGGTGGCCAGG
 AGTCCCCCTACTGCTGTGGGCTGGGGTGGGGGACAGCAGCCCCAGGCTGAGAGGCTGGAG
 CCGATGGCTAGTGGCTCATCCCCAGTGCATTTCTCCCCGTGACACAGAGAAGGGGCTTGGTA
 TTTTATTTAAGAAATGAAGATAATATTAATAATGATGGAAGGAAGACTGGGTTGACAGGGAC
 TGTGGTCTCTCTGGGGCGCGGACCGCGCTGGTCTTTACGCCACTGCTGATGACACACCC
 GTCCAGGCCAGACACCACCCCCACCCCACTGTGCTGGTGGCCCCAGATCTCTGTAATTTTA
 TGTAGAGTTTGAAGTGAAGCCCCGTATATTTAATTTATTTTGTAAACACAAA

FIGURE 70

MTPSPLLLLLLPLLLLGAFPPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTHSGWSRFRVLPQGLKVQVEREDAGVYVCKATNGFSLSVNYTLVVLDISP GK
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIA R PVGSSVRLKCVASGHRPDPITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPVL
TGTHPVNTTVDFGGTTSFQCKVRS DVK PVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLT VLPDPKPPGPPVASSSSA
TSLFPWPV VIGI PAGAVFILGTLLWL CQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS
LAALSAGPGVGLCEEHGS PAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHSTHSHVEGKV
HQHIHYQC

FIGURE 71

CCGAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAACTTCCCAGGGGACCGCATCCAGAGTCA
 AGTGACTCTGTGAAGCACCCACATCTACTCTTGCCACGTTCCCACGGGTCTGGGGGAAACATGGTGGGGACCA
 AGGCTGGGTGTTCTCCCTTCTGGTCTGGAAGTCACATCTGTGTTGGGAGACAGAGCATGCTCACCCATCA
 GTAAGAGAGTCCAGCCTGGGAGAGAAAGACCCAGCATCTTTGCCAAGCCTGCCACACCTCGGAGAGCCCTGG
 TGAGTGGACAACTGGTTCACATCGACTTCCCAGCGGGAGGGCACTATGAGCGCTGGACGCCATTCGCT
 TCTACTATGGGACCTGTATGTCCTCGCTCGCTGAGGCTCGGACCACTGATCGACACTCGGACACTCGGAG
 AGCATCGGCCAGCTGCTCATGTGATCTCCCGTGAGGGTTTCTGCTGCTTCAACAGGAGACAGCGCTCGGCCA
 GAACCTGCTCTAATTACACCTGACTGTTCTCTGCCACAGGATCCCTGGCGGAGACAGAGCGCATCTGTGA
 GCGCATGGTCTCCCTGGAGCAAGTGTCTGAGCTGCTGTGGTCACTGGGTCCAGACTCGCACACGCATATTGC
 TTGGCAGAGATGGTGTGCTGTGCGATGCGAGTGGGCGAGCGAAGGGTTCAGCATCTCATGGGCCAGGACTGTACAG
 CTGTGACCTGACCTGCCAATGGGCGAGTGAATGCTGACTGTGATGCTGTGATGTGGCCAGGACTTCATGCTTC
 ATGGGCACTGCTCTCTCCCTCGGAGAGTGGCCAGCTCAGGGCTGCTATCTTACTCTCGGACAGCGCGAG
 CTGCTGACCCAGACACAGACTGATGGGAGATTCCGAATCCCTGCTTGTGCCCTGATGGCAAAAGCATCTGAA
 GATCACAAGGTCAAGTTTGCCGCCATTGTACTCAAAATGCCAAGACTAGCTGAAGCGAGCCACCATCAAGG
 CAGAGTTTGTGGGGCAGAGACTCCATACATGGTGATGAACCTGAGACAAAAGACGAGAGCTGGGCGAGCG
 GTGTCTCTGTGCTGTGAAGGCCACAGGAGAGCCAGGCGCAGACAAGTATTTTGGTATCATATGACACATTTGCT
 GATCCTCTTCCCTTACAGCATGAGGACAAGCTGTGCTGAGGAACCTGCAGCAGACACTGGGCGAGTACT
 TTTGCAAGGCCAGCATGATCTGGGCTGTGAGTGTGCCAGCTTATTTGCACAGCATCTGATGAG
 ACTCTTGGCAACCACTCTCTGAGAGCTATCTTATCCGGCTGCCCCATGATGCTTTGAGATGGCCCAACTCT
 CTTCTACTATGACGTGGGACGCTGCCCTTTAAGACTTTGTGCGGCGAGCAGGATGATCCGAGATGACGCTG
 ATGCTGTGCGAGCACTCTGTGGCATCTCCAAGACAGAGGAAGGGAGATCCAGTGCAGTGGCTTACACGCTACCC
 ACCAAGGTGGCAAGAGGTGAGCTGCGAGCGGTGTACGGAACCTCGGAGCATCTGCTGGGGCGGTGTGACTGC
 TGTGACATTTGGGAGCCCATGCGCTTTGGCATGTGTCATGTGGGACACGCGCTGTAACTGATGCTGCTACAG
 AGGGCACTTTCCTTCCCTCATCTCCCGAGGACTGAGGCTGTGCTTATTTGAGAGGTGTGCAAGG
 TTTCTCAACACCAACCAAGTGTACTCTTCAACAAGAGGGGAGTCCGCTGTTCCATGAATCAAGTACTGCTG
 TCGGAAGAGGCCCATCACTTTGAAGCCATGGAGACCAACATCATCCCCCTGGGGGAAGTGGTTGGTGAAGACC
 CCATGGCTGAATCGAGATTCCATCCAGGAGTTTCTACAGCGAGAATGGGGAGCCCTACATAGGAGGTGAAG
 GCGCTGTGACCTTCTCGATCCCGGAATATTTCAACAGCCACAGCTGCCAGACTGACCTGAACCTTCAICAA
 TGACCAAGGAGCACTTTTCCCTTTCGAGCATTTGCGATTTCTCTGTGGACTTCAGAGATGAGGTCAAGCTAG
 AGCCCATTTATCTCTGCGAAAGTGAAGTCCACCTTGACTCCAGCAGTCAAGATGCCAGAGACACATATCCACA
 GTCAACTCTGTGTCATCAATCCAGACACAGGCTGTGGGAGGAGGAAGTGATTTCAAAATTTGAAATTCAAAG
 GAGGAACAAAGAGGAGACCAACCTTCTGTGGGCAACCTGGAGATTCTGTGAGAGGAGGCTCTTTAACTGCTG
 ATTTTCTGAAAGCGAGCGGTGCTTTGTTAAGGTGAGGGGCTTACCGGATGAGAGGTTCTTGGCTAGTGAGCAG
 ATCCAGGGGGTGTGATCTCCGTGATTAACTTGAGGCTGAGACTGCTTCTTCTGTCCAAACCTTAGGCGCTGGG
 CGCTTTTGAGGTGTATCTCGAGCGCCACAGGCGCTGTGCTCTGCTGTGATGACACTCCCTGATG
 CCTACTCTGCTTATCTTGTGCAAGCCTGGCTGGGGAGGAATGCAAGCAGTGGAGTCTTCTCTCAATTTCAAC
 CCAATGCAATTTGGCTGCCCTATCTCAACAAGCTCAACTACCGTGGGAGGAGCATGAGGATGCAAG
 GGTAAAGACAGCACTTTCCAGATTAGCATGGCCAGGCCAAGCCCACTCAGCTGAGGAGAGCAATGGGCCCA
 TCTATGCTTTGAGAACCTTCGGGCATGTGAAGAGGACCAACCCAGTGCAGCGCACTTCGGTTTCTTACCAGATT
 GAGGGGATCGATATGACTCAACAGACTCCCTTGACCAAGGATGACCTTATGAGCTGTGACTCAAGTCACT
 GGCATGTGTGGCCAAAGCCTGGAATTACGGCGCTGCTATATCAAGTGAAGATTCTGGGGCACTGGAAGTGA
 ATGTGCACTCCGCAACATGGGGGCACTCATCGCGGACAGTGGGGAAGCTGTATGAATCCGAGATCTGAGG
 AGCATCTGGGACAGGAGACAGCCCAATGCTCAGCTGCTGTGAGTTCAAGTGCAGTGGGATGCTCTATGA
 TCAGGACGCTGTGGGACCGCACTCTGGTGAAGTGCATCCCCAGGCGAGCTGCGCTGCAGGCTGCTTGAACCCCA
 TGCCTGATGAGTCACTGTGTCACCACTTGGCACTTGCAGTTCGAGTCAACAGCAGCCAGTGAGTACACATGCTGGCA
 CCTGTGACCTCACTGGGCGCACTATGCACTATGCACTCTCACTGAGCAGGCTCTGAGCAGCGCACTGAGAT
 CGCGCTCGCGCTGCTTTGATGSCACATCCGATGGCTCTCCAGGAATGAGAGGCAATGTGGAGTGAAGCC
 TCACCTTCAACTGTGTGAGAGGCAAGTAGGCGCGCAGAGTGCTTCCAGTCACTGCCAAGACAGCCAGCCAGC
 TCCCCCTGTCGAGGCACTGTGTCRAAGGAAGTGCCTCTGAGAGGCGAGCAGCGAGCGAGGGGTGGCCAGGC
 CGAGGTTGGAGTGTGGGCTCTCTGAGATTCTCTAGAGTTGCTCAACAGCCCTGATCAACTAAGTTTGTGGT
 ACTTCACCCCTTCTGGCTCATTTCACTGACAGGCATTTGAGACTGATGACAACTGCAACTGCTGCTTAAT
 TTARGACTTCTGTTCTGATTTGCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTG
 TTGGCACTGGTGGCCCAACATGGCCCAATAAAGCCCTTTGTGAACTGTTCTTTAAATGAACCAAGAAAT
 GGCCACTGGTAAACTCTGCAAGTCTCAACTGTACTTCAATTTAAATGCCAATATATCTTCTCTCTTCTTCTT
 TTTGCTGATGTTTGGCCACCTTGCATAAGTGATAATCTGATGCTGAAGATCAATAACCAATATAAGCATAT
 TTTTGGCGCTTGTCTCCAGCAGACATAGGCAAGCCTTGTATCATGTTTATACATATTAATGGTGGTGAATAAG
 AATAAARACATATCTTTACTTTGAATGTAAATACTTATTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
 ACATTCACCTTACGCTTAAATATAGGCTGATCATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
 AATCAATTAACACAGGTGCTCAACTGTATTTGTACATTTCCCTTGCATTGCTTGTGTTCTGCTAGAAAC
 CCAGTGTAGCCAGGGCAGATGTCAATAATGATACTCTGTATTTCGAAAAA

FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLES PGEWTTWFNI
 DYPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPREGFWCLNREQ
 RPGQNCNNTYRFLCPPGSLRRDTERIWSWPSPWSKSCAACGQTGVQTRTRICLAEMVSLCS
 EASEEGQHCHMGQDCTACDLTCMPMQVNADCDACMCQDFMLHGAVSLPGGAPASGAAIYLLTK
 TPKLLTQTDSGRFRIPGLCPDGKSIKIKITVKVFAPIVLTMPKTSLKAATIKAEFVRAETPY
 MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRKLQQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNVPVPEYLIIRLPHDCFQATNSFYDVGRCVPV
 KTCAGQQDNGIRCRDAVQNCCKGSKTEEREIQCSGYTLPTKVAKECSCQRCTETRSIVRGRV
 SAADNGEPMRFGHVYMGNSRVSMGTGYKGTFTLHVPQDTERLVLTFVDRQLQKFVNTTKVLPFN
 KKGSAVFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKV
 KASVTFLDPRNISTATAAQTDLNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRNRKREDRTFLVGNLEIRERRLFNL
 DVPESRRCFVKVRAYRSEFLPSEIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
 CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLNRYRTDHDPR
 VKKTAFAQISMAKPRPNSAEESNGPIYAFENLRACEAPPAAHFRFYQIEGDRYDNTVPFN
 EDDPMSWTE DYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLKVIPQGSRRASVNPMLHEYLVNHLPLAV
 NNDTSEYTMPLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTS DGSSRIMKSNVGVALT
 FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQQRASRGGQRQGQGVVASLRFPRVA
 QQPLIN

FIGURE 73

CTGCAAGTTGTTAACGCCATAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCAC
 AATATCTTAACTCTTCATATTTGGTTTTGGGATCGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAG
 ACCCTACCTACCCGTACGCATACATACATATGTATATATATGTTAACTAGACAAAGATCGCAGATCATAAAGC
 AAGCTCTGCTTTAGTTTTCCAAGAAGATTACAAAGAAATTAGAGATGATTTGTCAAGATCCCTGCTCGATTCATG
 CCGCTTTGGGTTACGCTGTCTCAGTGATCCAGCCCTACCTTTGGTTGGGGACATTTATGATTTGTTGAAGACT
 CAGATTTACACGGAAGAAGGAAAGTTTGGGATTACATGGCTGCCAGCCGGAATCCACGGACATGACAAATA
 TCTGAAAGTGAACCTCGATCTCCGGATATTACCTGTGGAGACCCCTCTGAGACGCTCTGTGCAATGGGCAATC
 CCTACATGTGCAATATGAGTGTGATGCGAGTACCCCTGAGCTGGACACCCCCCTGAGCTGATGTTGATTTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGGAGGAGTATCCCAAGCCTCTCCAGGTTAAACAT
 CACTCTGTCTGGAGCAAAACCATTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC
 AATGATCCTGGAGAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTCACATGGATCCTAAATCCGTGAAGGATTTATCACGACATACGGCTTAGAAATCATTTCACACAGA
 AGAGTACTCAACAGGATATACAACAAATAGCAAAATATCCACTTTGAAATCAAAGACAGGTTCCGCGCTTTTGT
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAACTCAGAGATTTCTTT
 ACAGTACAGACCTGAGGATAAGGCTGTTAAGACCAGCCGTTGGGAAATATTTGTAGATGAGCTACACTTGGC
 ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGAATCTCCATGCCACTGTATGTG
 TGTATGACAACAGCAAAATGACATGCGAATGTGAGCACAACACTACAGGTCCAGACTGTGGGAAATGCAAGAAG
 AATTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCATCCCCAAAGGCACTGCAAAATACCTGTATCCC
 CAGTATTTCCAGTATTTGGTACGAATGTCTGCGACAACGAGCTCTGCACTGCCAGAACGGAGGACGTTGCCACA
 ACAACGTGCGCTGCTGTGCCCGGCCGATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGC
 AGCTGCGGCTCCGACTCTGGCCAGGGCGCGCCCCGCGACGGCACCCAGCGCTGCTGCTGCTGACACGCTGCT
 GGGAAACCGCCAGCCCCCTGGTGTCTTAGTGTACCTCCAGCCACACCGGACGGCCGTGTGCGGTGGGGAAGCA
 GACACAACCCAAACATTTGCTACTAACAATAGGAACACACACATACAGACACCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCCATACTGAACATAAGCCATATTTATCACCCGTGGACAGCACATCCGACTCAAGACTTAAATTTT
 TGACTCCAGAGGAGTTGGCAGCTGTGTATATTATCACTGCAAAATCACATTTGCCAGCTCGAGAGCATATTGTGGA
 TTGGAAAGGCTGCGACAGCCCCCAACACAGGAAGACAAAAACAAACAAATCAACCGACTTAAACATTTGGC
 TACTCTAGCTGGTGGCGCCCTAGTACGACTCCGCCAGTGTGTGGACCAACCAATAGCATCTTTGCTGTGAG
 GTGCATTTGGGCAATAGGAATCTGTTACAGCTGCCATATTGGCTGCTTCGTCCTCCGTAATCCCTTCCAAC
 CTGGCTTTTATGTAACGTTGCTCTGTAAACCTCGTTGGTTGAAAGATTCTTTGTCTGATGTTAGTGATGCACA
 TGTGTAAACGCCCTCTAAAGCGCAAGCCAGTCTATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGGCA
 GCACACCCCACTATACAAGAGTGGCTATAGGAAAAAGAAAGTGTATCTATCCCTTTGTATTCAATGAAGTT
 ATTTTCTTGAACACTGTAATATGTAGATTTTGTATTATTGCCAATTTGTGTTACAGACAATCTGTTAAT
 GTATCTAATTCGAATCAGCAAGAAGTACATTTTATTTGCTCCTCTTCGTTCTGTTTGTTCCTGTGCGAGA
 GATTTCTGTGAAGGCAAGCAAGTGTGTCATCAAGAATATCAGTTTACATATATAACAAGTGAATAAGA
 TTTCCACCAAGGACATCTTAAAGTTTTCTTGTTGCTTTAACTCGGAAGATTAAAGAATAAAACCTCTGCA
 TAAACGATTTTCGGAATTTGATTGCAATTTCTTAAGTGAAGGAACAGCCACCAAGCAATTTTCACTACT
 TTACTGATTTCTGTGGGACTGAGTACATTCAGCTGACGAATTTAGTTCCCGAAGATGAGTTGATGATGTTCACT
 AGCTTGGACAACTTTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTAACAACAGCAAAAAA
 AAAAAA

FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
 VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
 EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMILEKSLDYGRWTWQPYQYYATDCLDAF
 HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
 TTKKLRDFFTVDLRIRLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
 SKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPPIPKGTANTCIPSISSIGTNVCDNELLH
 CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTLLGTAS
 PLVF

FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTCCGGCTAAGATTGCTGAGGAGGCGG
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGCCGCGCTCCGGGCGAGGTGTCTCATGACTT
 CTCTTGCGACCATGTCCGTGATCTTTTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAAGATTTTTTGGAAATGGAGGAGACGGCTCA
 AGAGTTTAGCCTTGCGACTGGCCAGTATCCAGGTGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACATTTTTCTTCTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTTCTGCTTCTTGAGACCCGTGGTGGGAATTCACAGCTTCCTATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTAG
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAATAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGATGAATGGTCACACCCGATGCACTTGGAGCCTGCTCCTAATTTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT
 CATTTCGAGGAGTTCACCTTGCAGAACATTTTACAGGATCCAAGGAGCTGGTTCCTGCTGGT
 TGGACCAAACCTCGTGAGCCAGCCACCCCTGACCCAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGAAATCTCATCAGCAGGAGCCTGTGGA
 AAAGGGCATGTCAAGTGAATCTGGGAATGGCTGGATTCCGAAACATCTGCCATGTGTATTG
 ATGGCAGAGCTGTTGCCACAAGCGCCTTTTATTTAGGGTAAATTAACAAATCCATTCTAT
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCTTACATTTATATGATTCTGGGGTT
 GCTTCAGAAGTGTTATTTTCATGAATCATTCATATGATTGATCCCCAGGATTCATTTTGT
 TTAATGGGCTTTTCTACTAAAGCATAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT
 TTACTTTACATATTCGTTTTCAATACTTGTGTTTCATGTTACACAAGCTTCTTACGGTTTTT
 TTGTAACAATAAATATTTTGTAGTAAATAATGGGTACATTTTAAACAACTCAGTAGTACAACC
 TAAACTTGTATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATTAATG
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAACAAAAAAAAAAAAAAAAAA
 AAAAG

MSVIFFAFCVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIH
SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTTCIGLASRPYAFLEFDSIIQVKV
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLRGVHLAEHSLQDPRSWFCWLDQTS

TGCTTCCTGGAGACCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
 AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTACAGAAAGTGAAGTGGCATT
 TTAACATATGAAGTTCCTNTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAG
 TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAAATGGGGT

FIGURE 78

CTCAGCGGCGCTTCTCGTAGCGAGCCTAGTGGCGGGTGTGTCATTTGAAACGTGAGCGCGA
 CCCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAACGAGGCGGGTGGTG
 CCTGCCCCCTTAAAGGGCGGGCGCTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTT
 TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGCGGGCGCTT
 CCTCCCCGCTCGTCTCTCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA
TGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC
 GAGTGATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCTGTAC
 CCGCTTCAAGAAGCCTGCTGAGTTACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA
 TTGCGCTCGAGCTGTGCACCTTTACCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCC
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCGGAACACTACATCCAGTGGCT
 CAACGGCTCCCTCATCCATGGCTCTGGAACTTGTGTTTCTCTTCCCCAACCTGTCCCTCA
 TCTTCTCATGCCCCTTGCATATTTCTTCACTGAGTCTGAGGGCTTGTCTGGCTCCAGAAAG
 GGTGCTCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGTCTGGTGCT
 AGGTATGGTGTTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
 ATGACTTTTGGGAGTACTATCTCCCTACCTCTACTCATGCATCTCCTTCTTGGGTTCTG
 CTGCTCCTGGTGCTACTCCATGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG
 CAGCCCTGACCCCGCAGGATCTGTAATCCTACTTCTGCTGGCTGCCCTTAGACATGGAGCTG
 CTACACAGACAGGTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGGCGGAAGGC
 TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTCTGGTGCTACCGG
 GCCTGTCTGTGCTCATTGTGGCCATCCACATCTGGAGCTGCTCATCGATGAGGCTGCCATG
 CCCCAGGGCATGCAAGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
 TGCCGTCATTCAAGTTGACTCATCTTTTACCTAATGGTGCTCAGTTGTGGGCTTCTATA
 GCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCAGCACTGCCATGACGCAGATAATT
 GGAACCTGTGTCTGTCTCTCTGCTTAAGCTCAGCACTTCTGTCTTCTCTCGAACCTGGG
 GCTCACTCGCTTTGACCTGCTGGGTGACTTGGACGCTTCAACTGGCTGGGCAATTTCTAC
 TTGTGTTCTCTACAACGCAGCCTTTGCGAGGCTCACCACACTGTGTCTGGTGAAGACCTTC
 ACTGCAGCTGTGCGGGCAGAGCTGATCCGGCCCTTTGGGCTGGACAGACTGCCCTGCCGT
 CTCCGGTTTCCCCAGGCATCTAGGAAGACCCAGCACCAGTGACACTCCAGCTGGGGTGGGA
 AGGAAAAAAGTGGACACTGCCATCTGCTGCCTAGGCTGGAGGGAAGCCCAAGGCTACTTGG
 ACCTCAGGACCTGGAATCTGAGAGGTTGGTGGCAGAGGGGAGCAGAGCCATCTGCATATT
 GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCTGCTTTTCCATACTTAACTGTGGCT
 CAGCATGGGGTAGGGCTGGGTGACTGGGCTAGCCCTGATCCCAAAATCTGTTTACACATCA
 ATCTGCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTTGATGTGCAAT
 AGGGTGGGTAGGGGCAAGGAAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC
 TCTGCCTCTGGCCAGCAGACCTAAGCACTGTGCTATCTGGAGGGCTTTGGACCACCTC
 AAAGACCAAGGGATAGGGAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCAGGGA
 AAAAA

FIGURE 79

MEAPDYEVLVSVREQLFHERIRECIISTLLFATLYILCHI FLTRFKKPAEFTTVDDDEDATVNK
 IALELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYIQWLNGLIHGLWNLVFLFPNLSL
 IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
 YDFWEYYPYLYSCISFLGVLLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEEQLYCSAFEE
 AALTRRICNPTSCWLPDMELLHRQVLALQTQRVLEKRRKASAWQRNLGYPLAMLCLLVLT
 GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLGSGFQAVIQVVLIFYLMVSSVVGFY
 SSPLFRSLRPRWHDAMTQIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLGIFY
 IVELYNAAFAGLTTLCLVKFTFTAAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

FIGURE 80

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC
GCTCGTCCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAAACGAGGCGGTGGTGC
 CTGCCCCTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC
 TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGCGGCTTCCT
 CCCCCTTGTCTNTCCCGGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
 AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
 GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
 TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
 GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCT
 CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTC**ATG**CTGCTGT
GGGTGATATTACTGGTCTGGCTCCTGTCAGTGGACAGTTTGCAAGGACACCCAGGCCCAT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA
GGGATTTCGCTTCTACTCACCAAGAAAACAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAAGGAATCTGGAGAGTACAGATGCCAG
GCCAGGGCTCCCCTCTCAGTAGCCCTGTGCACTTGGATTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACC**TAG**GCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCTGGCATTCCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 83

MLLWVILLVLAPVSGQFARTPREIIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSEMGFPHAAQANVELLGSSDLLT

FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCGCGCCCCCGGTGT
 GAGGCGGCCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGAGGAGGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGCTCCGCAGAACCTGAGCACCTTTT
 GCCTGTGTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG
 GGGGTGCCTCGAAGTGCCTCTATAAAGGATATTTAAAAAGGCCTATAGGAAACTAGCCCTGCA
 GCTTCATCCCAGCCGAACCCCTGATGATCCACAAGCCAGGAGAAATTCAGGATCTGGGTG
 CTGCTTATGAGTTCTGTGAGATAGTGAGAAACGAAACAGTACGATACTTATGGTGAAGAA
 GGATTTAAAGATGGTTCATCAGAGCTCCCATGGAGACATTTTTTACACTTCTTTGGGGATTT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCGAAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGAGGCTCCTGGCAAACGGAAGTGCAATTGTGCGCAAGAGAT
 GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
 AGATTTACGGTCCGAATCAAAGTTGTCAAGCACCCCAATATTTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA
 TCACTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTCAGAGTG
 AATAAAATTTGACTTTGTTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGTTTTT
 TTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTGTCATTGCGAAAAGAATGACC
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCTGAGT
 TTCAAGATTTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAACACAATATAGAGGTTTGA
 GTTGTTAGCAATTTCAATCAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTG
 TTATTTTTTA

FIGURE 85

MAPQNLTFCLLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKALQLHPDRNPDDPQ
 AQEKFQDLGAAYEVLSDSEKRRQYDTYGEGLKDGHQSSHGDI FSHFFGDFGFMFGGTPRQQ
 DRNIPRGSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTQLGPGRFQ
 MTQEVVCDECPNVKLVNEERTLEVEIEPGVRDGMETPFIGEPEPHVDGEPGDLRFRIKVVVKH
 PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHISRDKITRPGAKLWKKGEGLPNFD
 NNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
 GCGGCGGGCGGAGGAGGTTTTTGAGGATTTTTGGAACAGGACCCGGACAGAGGAACCATGGTT
 CCGCAGAACNTGAGCACNTTTTGCCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
 ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTAAAAAGG
 CCTATAGGAAACTAGCCCTGCAGNTTTATCCCGACCGGAACCTGATGATCCACAAGCCCAG
 GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAACA
 GTACGATAATTATGGTGAAGAAGGATTAAGATGGTNATCAGAGCTCCCATGGAGACATTT
 TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
 AATATTCCAAGAG

FIGURE 87

GGCACGAGGCGGCGGGGCAGTCGCGGGATGCGCCCGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCCTGCAGGTGCTGCTGGAGAACCTAGCACCTGCCATCCTCTTCCCAATTTGCCACTTCCA
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGATGAGTCAGGAGCCCTCTGGAAGC**ATGG**
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGCAGCC
 TTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATTTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
 TGGACGATGTCGTTATACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGAC
 AGAGAAGCTTGTGGCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTGTGGTGCCAAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCCTCCGTTGGACCCCAAACCTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGAG
 TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACC
 AGTCTCTGTGCGGCTGCTGAGGAGCATTGGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
 CCAGATAAAGGCCTCCCAGGCCTGAAGGCTTCTGACAGGAGCAGTCTGCAATT**TAGT**GCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCGGCCATCCCTGGATGGCTCAGCTTAGCCTT
 CTACTTTTTCCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTCATAG
 TAAAGCAGGAGATCCCCGTCAGTTTATGCCTCTTTTGCAAGAGGAGTATTGAAAA
 CTGGTGGACTGTCAGCTTTATTTAGCTCACCCTAGTGTTTTCAAGAAAAATTGAGCCACCGTCT
 AAGAAATCAAGAGGTTTACATTAAATTAGAATTTCTGGCCTCTCTCGATCGGTCAGAATG
 TGTGGCAATTTCTGATCTGCATTTTCAGAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC
 TTCTTTTGGCAAGACTTGACTCTCTCACCTGGCCTGTTTCATTATTTGTATTATCTGCCT
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGACAGTTTGGGTTTGAAGCTGAGGAAC
 ACAAAAGTTGATGATTTCTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
 GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAA

FIGURE 88

METVTVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSSEL
 ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTLEKLVAMTMGSGAKMKTAS
 VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLLSVSHLVLVTRNACHLTGGLDWI
 DQSLSAEEHLEVLREAAALASEPDKGLPGPEGFLQEQSAI

FIGURE 89

GCTTCATTTCTCCCGACTCAGCTTCCACCCCTGGGCTTCCGAGGTGCTTTCGCCGCTGTCC
 CCACCACTGCAGCC**ATG**ATCTCCTTAACGGACACGCAGAAAAATTGGAATGGGATTAACAGGA
 TTTGGAGTGTTTTTCCCTGTTCTTTGGAATGATTCTCTTTTGGACAAAGCACTACTGGCTAT
 TGGAAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAAATGGTTTAGAAGAACATTTCAGAT
 TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGGTGGTGATTTGTAGTC
 CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTTGTTTCTCAG
 GGGCTTCTTTCCCTGTCGTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
 TTACCTGGAATTAGATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTAT**TAA**CAACA
 AGTGAATTTGAAGACTCATTTAAATATTGTGTTATTATATAAAGTCATTTGAAGAATATTCA
 GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAACGTATAG
 CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAAAGGCTTCTACTCAAGTGA
 ACTAAGAAGAAGTCAGCAAGCAAACCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
 ACTCTTGAAGGCTATTTGTGTTGTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
 CTGTGGTGCCGTGTTCTTTCTTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
 TTTTAGAAGTGCTCACTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA
 TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAACCAAGGAAACCCCAATTTTG
 ATGTATGGATTACTTTTTTTTGNGCNCAGGGCC

FIGURE 90

MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK
 HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRRVPLGSLNLNPGI
 RSFVDKVGESNNMV

Important features:**Transmembrane domains:**

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCGACTCAGCTTCCC
 ACCNTGGGCTTTCCGAGGTGCTTTGCGCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
 CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTGGAGTGTTTTCTGTCTTTGGA
 ATGATTCTCTTTTTGACAAAGCACTACTGGCTATTGGAATGTTTTATTGTAGCCGGCTT
 GGCTTTTGTAATTGGTTTAGAAAGAACATTGAGATTCTTCTCCAAAAACATAAAATGAAAG
 CTACAGGTTTTTTCTGGTGGTGTATTTGTAGTCCTATTGGTTGGCCTTTGATAGGCATG
 ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

FIGURE 92

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
 GGCTGCCAGGAAGGAGACGCCITCCTGAGTCCCTGGATCTTTCTTCTCTCGGAAATCTTTGA
 CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGC
 TGAAGTCTCAGTTCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCTCAGGGCTAATC
 ATCAACACCATTACGTCTTCACTCTCCTCCTCTGGCCATTAAACAAGCAGCTCTTCCGGAA
 GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
 CGGGCACGGAATGCACCATCTTACGGACCCGCGCGCTACCTCAAGTATGGGAAGGAAAAT
 GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
 ACGCTTTGGGCTGTAGGGGGCTCCAAGGTCTGGCCAAGAAAGAGCTGGCCTATGTCCCAA
 TTATCGGCTGGATGTGGTACTTACCGAGATGGTCTTCTGTTCCGCAAGTGGGAGCAGGAT
 CGCAAGACGGTTGCCACCAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTCTCT
 GATTCACTGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
 GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
 ACCGTGAGGAGCTTGAGAAATGTAGTTTACAGCTGTATATGACTGTACACTCAATTTCAGAAA
 TAATGAAAATCCAACACTGCTGGGAGTCTTAAACGGAAAGAAATACCATGCAGATTTGTATG
 TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCCTGGCTGCAC
 AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGA
 GACGCCATGGTGCCCCCGCGCGCCCTGGACCTCGTGAACCTGGCTGTTTTGGCCCTCGC
 TGGTGCTCTACCCCTTCTTCCAGTTCTTGGTCTGATGATCAGGAGCGGGTCTTCCCTGACG
 CTGGCCAGCTTCATCTCGTCTTCTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
 GACGGAATTTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGGAGGTGTACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCT
 CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCCCTGCTGGGCACGGCGGAAGTACGA
 CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGGATGGGAGGAAGATGTTTTGTAATCTTT
 TTTTCCCCTATGTCTTTAGTGGGCTTTGGTTTTCTTTTGTGCGAGTGTGTGTGAGAATGGC
 TGTGTGGTGAGTGTGAACTTTGTCTGTGATCATAGAAAGGTATTTTAGGCTGCAGGGGAG
 GGCAGGGCTGGGGACGAAGGGGACAAAGTTCCTTTTATCTTTGGTGTGAGTTTTCTGT
 AACCTTGGTTGCCAGAGATAAAGTGAAAAGTGCTTTAGGTGAGATGACTAAATTTATGCCTC
 CAAGAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAAAA

FIGURE 93

MDLAGLLKSQFLCHLVFCYVFITASGLIINTIQLEFTLLLPINKQLFRKINCRLSYCISSQLV
MLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHNKFEIDFLCGWSLSERFGLLGGSKVLAKK
ELAYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHLLPRTKGFATVRSRLRNVVSAVYDCTLNFRNNENPTLLGVNLGKK
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTGTFETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVWRWMIGVTEIDKGSAYGNSDS
KQKLND

FIGURE 94

CTGAGGCGCGGTAGCAT**ATG**GAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAA
 GTAAAGGTGAAGCCAAGAACAGCATTACTGATCCCAAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATTCGGTCGTCATTGATCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAAGTTGACAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAAACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCCTATATAAAACCTCAAAAAGGACTT
 TTTACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACTGGGTTATAAAAC
 TGTATCAGGTTCCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAACACACAGCTCTAAAT
 TTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAGAGATATATGCAAAAAAGTGGGAAGCAGTGAAACAAGCAGTAGATAAACT
 AGTAAAGGATGTAAACAGATTAAAACGAGAAATTGAGAAAAGGAGAGGAGCAGAGATTCAGG
 CAGCAAGAGAGAAGAACATCCAAAAAGACCTCAGGAGAACATTTTTCTTTGTGACGGCATT
 CGGACCTTTTTTCCAAATTCGAATTTCTTCATTATGTTGTTATGTCTTTAAAAAATAGACA
 TGTTTCTAAAAGTAGCTGTAACATAACCACCATCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACA
 TTT**TGA**TCCTTTTAAACCTTACAAGGAGATTTTTTATTGGCTGATGGGTAAAGCCAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTGTTTTTACTATGTTAC
 CTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAAC
 ATCAGATGCTTTTATTCCAAACCTTTTTTTCACCTTTCACCTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCCGACCTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCACGATATTGAGACCATGCTATTAATAAATAAATGAAAAGCAAGAATAGCCTTAT
 TTTCAAATATGAAAAGAAATTTATATGAAAATTTATCTGAGTCATTAAATTTCTCCTTAAG
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLEVKGEAKNSITDSQMDDVEVVYTIIDQ
 KYIPCYQLFSFYNSSGEVNEQALKKILSNVKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH
 FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGKTVSGSC
 MSTGFSRAVQTHSSKFFEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
 RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS
 CNYNHHLDVVDNLTLMEHTDIPEASPASTPQIIKHKALDLDLRWQFKRSRLLDTDQKRKA
 NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

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FIGURE 96

GGCCAGCGCGCGGGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCGAGCGCAGGGCAGC
 CCAAGCAGCGCGCAGCGAAGCGCCGCGCCGCCACACCTCTCGGGTCCCCGCGGGCGCTGCCACCCCTTCCCT
 CTTTCCCCGCGTCCCCGCTCGCCGGCCAGTCAGCTTGC GG GTTCGCTGCCCGCAGAACCCCGAGGTACCA
 CGCCGCGCTCTGCTTCCCTGGCGCGCGCGCGCTCCAGCCCTCCTTCTCCCTGGCCGCGCGCTGGCAAC
 GGGGACCGTTCGCTCAGCGCAGGCGCCAGCTCTACTTTTCCCGCCGCTCTCTCCGCTGCTCGCCTCTCCAC
 CAATCCAACTCCTTCTCCCTCCAGCTCCACTCGCTAGTCCCGGACTCCGCCAGCCCTCGGCCGCTCGCGTAG
 CGCGGCTTCCCGTCGGTCCCAAAGTGGGAACGCTCGGCCCGGCCCGCACCTGCGACCGGTTCCGGCTTGGC
 CGCGCTTCTCTGCACCTGGCAGTGCTCAGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGG
 AAGTGCAGCTCTTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCAT
 TTGAAGATCTGTCCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTCGAAAAGTAAAGA
 TGATTTCAAAGTGTGTGTCAGCGAACAGTGCATCATTTGCAAGCTGTCTTTGCTTACGTTTACAAGAAAGTTG
 ATGAATCTTTCAAAGAACTACTTGAAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCAT
 TTATACATGCAAAATTTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT
 GAACCTGGAGAAGATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCGCCCTGGTGAACCTCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCT
 CGCAAATTTGAAGCTCCAGGTTACTCGTGCTTTGTAGCAGCCGTACTTTTCGCTCAAGGCTTAGCGGTTGCGGG
 AGATGTCTGTGAGCAAGTCTCCGTGGTAAACCCACAGCCGAGTGTACCCATGCCCTGTTGAAGATGATCTACT
 GCTCCCACTCGCGGGGTCTCGTGACTGTGAAGCCATGTTACAACTACTGCTCAAAACATCATGAGAGGCTGTTTG
 GCCAACCAAGGGATCTCGATTTTGAATGGAACAAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCCTTTCAACATTGAATCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAAG
 ATAAATAGTGTCAAGTGTCTCAGAAGGTTTCCAGGGATGTGAACCCCAAGCCCTCCACAGCTGGACGAATTT
 TCTCGTTCCATCTCTGAAAGTGCTTTCAGTGCTCGCTTCAGACCAACATCACCCGAGGAACGCCCAACCAACAGC
 AGCTGGCACTAGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAACAGGCCAAGAAATTTCTGTCCT
 CCCTTCGAGCAACGTTTGAACAGATGAGAGGATGGCTGCAGGAACCGCAATGAGGATGACTGTTTGAATGGG
 AAAGGCAAAAGCAGGTACTGTTTGCAGTGACAGGAATGATTAGCCAACAGGGGCAACCCAGAGGTCCA
 GGTGACACAGCAAAACAGACATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGA
 AGAATGCATACAATGGGAACAGCTGGACTCTTTGATATCAGTGATGAAAGTAGTGGAGAGGAAGTGGGAAT
 GGCTGTGATATCAGCAGTGCCCTTCAGAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGGCAATGA
 GAAAGCGCAGCTGCTGGTGCCGTCCTGGGGCAGCGCCCTACCTCTCTACTGTCTTCGATCTTGTTCCTCGG
 TTATGCAGAGAGAGTGGAGTAAATTTCTCAAACCTCAGAAAAGTGTTCATCAAAAAGTTAAAGGCACCAAGT
 ATCACTTTCTACCATCTAGTGACTTTGCTTTTAAATGAATGGACAACATGTACAGTTTCTACTATGTGGC
 CACTGTTTTAAAGAGTGCTGACTTTGTTTTCTCATTCAAGTTTTGGGAGAAAGGACTAGTCTGATGAGTTGGC
 TCCGTCTCCCCAAACCATGTTAAAGCTGGCTAACAGTGTAGGTACAGACTATAGTTGTTGTGCTTTGTGA
 TTTTATCACTCTATTTATTTGTTGATGTTTTTCTCATTTTCGTTTGTGGGTTTTTTTTCCCACTGTGATCT
 CGCCTTGTTCCTTCAAGCAAAACAGGTCCTTCTTGGCAGTAAACATGTACGTATTTCTGAAATATTAATA
 GCTGTACAGAGCAGGTTTTATTTATCATGTTATCTTATTAAGAAAAAGCCCAAAAGC

FIGURE 97

MARFGLPALLCTLAVLSAALLAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
 GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
 VKTYGHLYMQNSSELFKDLFVELKRYVVGNNLEEMLNDFWARLLERMFLVNSQYHFTDEY
 LECVSKYTEQLKPFQDVPRKLQVTRAFVAARTFAQGLAVAGDVVSKSVVNPTAQCTHAL
 LKMIYCSHCRGLVTVKPCYNYSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIES
 VMDPIDVKISDAIMNQDNSVQVSQKVFQGGCPPKPLPAGRISRSISESAFSARFRPHHPEE
 RPTTAAGTSLDRLVTDVKEKLQAKKFWSLPSNVCNDERMAAGNGNEDDCWNGKGKSYLF
 AVTGNGLANQGNNPEVQVDTSKPDILLRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE
 GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
 GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
 GCAACTTACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
 TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC
 AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
 AGATTGGTTCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGC
 AGTGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA
 AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
 TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAACATTCTCAGCCAAGAA
 GACAGTGAGCACCTACCAGACACTCTTCTTCTCCCACTCACTCTCCACTGTACCCACC
 CCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTCAAGATCATTTTGTTTGTGCTCTC
 TCTAGTGCTCTTCTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTT
 AATTACCTGAAAGATTCAGGAAACTGTAGCTTCTAGCTAGTGTCAATTTAACCTTAAATGC
 AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAA

FIGURE 99

MKVLISLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQCPDHFKGNVKKTRHQREHRKPNKHSRACQQLKQCQLRSFALPL

FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTTCATCAAAGTGAATCATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAAACAGAATCATTGAAACACC
CTGACTGCATTTTTGCTTTTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA

1. *Chlorophyll a* (Chl *a*)
 2. *Chlorophyll b* (Chl *b*)
 3. *Chlorophyll c* (Chl *c*)
 4. *Chlorophyll d* (Chl *d*)
 5. *Chlorophyll e* (Chl *e*)
 6. *Chlorophyll f* (Chl *f*)
 7. *Chlorophyll g* (Chl *g*)
 8. *Chlorophyll h* (Chl *h*)
 9. *Chlorophyll i* (Chl *i*)
 10. *Chlorophyll j* (Chl *j*)
 11. *Chlorophyll k* (Chl *k*)
 12. *Chlorophyll l* (Chl *l*)
 13. *Chlorophyll m* (Chl *m*)
 14. *Chlorophyll n* (Chl *n*)
 15. *Chlorophyll o* (Chl *o*)
 16. *Chlorophyll p* (Chl *p*)
 17. *Chlorophyll q* (Chl *q*)
 18. *Chlorophyll r* (Chl *r*)
 19. *Chlorophyll s* (Chl *s*)
 20. *Chlorophyll t* (Chl *t*)
 21. *Chlorophyll u* (Chl *u*)
 22. *Chlorophyll v* (Chl *v*)
 23. *Chlorophyll w* (Chl *w*)
 24. *Chlorophyll x* (Chl *x*)
 25. *Chlorophyll y* (Chl *y*)
 26. *Chlorophyll z* (Chl *z*)
 27. *Chlorophyll aa* (Chl *aa*)
 28. *Chlorophyll ab* (Chl *ab*)
 29. *Chlorophyll ac* (Chl *ac*)
 30. *Chlorophyll ad* (Chl *ad*)
 31. *Chlorophyll ae* (Chl *ae*)
 32. *Chlorophyll af* (Chl *af*)
 33. *Chlorophyll ag* (Chl *ag*)
 34. *Chlorophyll ah* (Chl *ah*)
 35. *Chlorophyll ai* (Chl *ai*)
 36. *Chlorophyll aj* (Chl *aj*)
 37. *Chlorophyll ak* (Chl *ak*)
 38. *Chlorophyll al* (Chl *al*)
 39. *Chlorophyll am* (Chl *am*)
 40. *Chlorophyll an* (Chl *an*)
 41. *Chlorophyll ao* (Chl *ao*)
 42. *Chlorophyll ap* (Chl *ap*)
 43. *Chlorophyll aq* (Chl *aq*)
 44. *Chlorophyll ar* (Chl *ar*)
 45. *Chlorophyll as* (Chl *as*)
 46. *Chlorophyll at* (Chl *at*)
 47. *Chlorophyll au* (Chl *au*)
 48. *Chlorophyll av* (Chl *av*)
 49. *Chlorophyll aw* (Chl *aw*)
 50. *Chlorophyll ax* (Chl *ax*)
 51. *Chlorophyll ay* (Chl *ay*)
 52. *Chlorophyll az* (Chl *az*)
 53. *Chlorophyll aza* (Chl *aza*)
 54. *Chlorophyll abz* (Chl *abz*)
 55. *Chlorophyll acz* (Chl *acz*)
 56. *Chlorophyll adz* (Chl *adz*)
 57. *Chlorophyll aez* (Chl *aez*)
 58. *Chlorophyll afz* (Chl *afz*)
 59. *Chlorophyll agz* (Chl *agz*)
 60. *Chlorophyll ahz* (Chl *ahz*)
 61. *Chlorophyll aiz* (Chl *aiz*)
 62. *Chlorophyll ajz* (Chl *ajz*)
 63. *Chlorophyll akz* (Chl *akz*)
 64. *Chlorophyll alz* (Chl *alz*)
 65. *Chlorophyll amz* (Chl *amz*)
 66. *Chlorophyll anz* (Chl *anz*)
 67. *Chlorophyll aoz* (Chl *aoz*)
 68. *Chlorophyll apz* (Chl *apz*)
 69. *Chlorophyll aqz* (Chl *aqz*)
 70. *Chlorophyll arz* (Chl *arz*)
 71. *Chlorophyll asz* (Chl *asz*)
 72. *Chlorophyll atz* (Chl *atz*)
 73. *Chlorophyll auz* (Chl *auz*)
 74. *Chlorophyll avz* (Chl *avz*)
 75. *Chlorophyll awz* (Chl *awz*)
 76. *Chlorophyll axz* (Chl *axz*)
 77. *Chlorophyll ayz* (Chl *ayz*)
 78. *Chlorophyll ayz* (Chl *ayz*)
 79. *Chlorophyll azz* (Chl *azz*)
 80. *Chlorophyll azaa* (Chl *aza*)
 81. *Chlorophyll abz* (Chl *abz*)
 82. *Chlorophyll acz* (Chl *acz*)
 83. *Chlorophyll adz* (Chl *adz*)
 84. *Chlorophyll aez* (Chl *aez*)
 85. *Chlorophyll afz* (Chl *afz*)
 86. *Chlorophyll agz* (Chl *agz*)
 87. *Chlorophyll ahz* (Chl *ahz*)
 88. *Chlorophyll aiz* (Chl *aiz*)
 89. *Chlorophyll ajz* (Chl *ajz*)
 90. *Chlorophyll akz* (Chl *akz*)
 91. *Chlorophyll alz* (Chl *alz*)
 92. *Chlorophyll amz* (Chl *amz*)
 93. *Chlorophyll anz* (Chl *anz*)
 94. *Chlorophyll aoz* (Chl *aoz*)
 95. *Chlorophyll apz* (Chl *apz*)
 96. *Chlorophyll aqz* (Chl *aqz*)
 97. *Chlorophyll arz* (Chl *arz*)
 98. *Chlorophyll asz* (Chl *asz*)
 99. *Chlorophyll atz* (Chl *atz*)
 100. *Chlorophyll auz* (Chl *auz*)
 101. *Chlorophyll avz* (Chl *avz*)
 102. *Chlorophyll awz* (Chl *awz*)
 103. *Chlorophyll axz* (Chl *axz*)
 104. *Chlorophyll ayz* (Chl *ayz*)
 105. *Chlorophyll ayz* (Chl *ayz*)
 106. *Chlorophyll azz* (Chl *azz*)
 107. *Chlorophyll azaa* (Chl *aza*)
 108. *Chlorophyll abz* (Chl *abz*)
 109. *Chlorophyll acz* (Chl *acz*)
 110. *Chlorophyll adz* (Chl *adz*)
 111. *Chlorophyll aez* (Chl *aez*)
 112. *Chlorophyll afz* (Chl *afz*)
 113. *Chlorophyll agz* (Chl *agz*)
 114. *Chlorophyll ahz* (Chl *ahz*)
 115. *Chlorophyll aiz* (Chl *aiz*)
 116. *Chlorophyll ajz* (Chl *ajz*)
 117. *Chlorophyll akz* (Chl *akz*)
 118. *Chlorophyll alz* (Chl *alz*)
 119. *Chlorophyll amz* (Chl *amz*)
 120. *Chlorophyll anz* (Chl *anz*)
 121. *Chlorophyll aoz* (Chl *aoz*)
 122. *Chlorophyll apz* (Chl *apz*)
 123. *Chlorophyll aqz* (Chl *aqz*)
 124. *Chlorophyll arz* (Chl *arz*)
 125. *Chlorophyll asz* (Chl *asz*)
 126. *Chlorophyll atz* (Chl *atz*)
 127. *Chlorophyll auz* (Chl *auz*)
 128. *Chlorophyll avz* (Chl *avz*)
 129. *Chlorophyll awz* (Chl *awz*)
 130. *Chlorophyll axz* (Chl *axz*)
 131. *Chlorophyll ayz* (Chl *ayz*)
 132. *Chlorophyll ayz* (Chl *ayz*)
 133.

FIGURE 101

MAVLVLR LTVVLGLLVFLTCYADDKPKDPDDKPDGSKDPKPDFPKFLSLLGTEIIENAVE
FILRSMRSTGFMEDDNEGKHSSK

FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
 CAGAGCTGGTCTGCCATGGACATCCTGGTCCCACCTCCTGCAGCTGCTGGTGCTGCTTCTTAC
 CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCC
 CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
 CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGCCCTACTGGAGCTGGG
 CTGCGGAAACGGAGCCAACCTTTCAGTTCTACCCACCGGCTGCAGGCTCACCTGCCCTAGACC
 CAAATCCCCACTTTGAGAAGTTCTTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
 GGTGGTCTGCACTCTGGTCTGTGCTCTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCC
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA
 AGCTGGGCCTTCATGTGGCAGCAAGTTTTTCGAGCCACCTGGAACACATTGGGGATGGCTG
 CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAAGCCCCAGTTCTCCGAAATCCAATAG
 AACGACAGCCCCCTCCCTTGAAGTGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTCT
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTGCTCCTTCCCCAGCCTCCAATTAGAACA
 AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTTAGCAGAATGAGAGAAGACATT
 CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
 CGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
 TGTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCTCCCAATGTTGTC
 CCTTTCTCTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCTGAGGCTACACCCATGCGT
 CTCTAGGAAGTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCCTCT
 CTCCCCACTACCACCTTCTTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA
 AACCACG

Figure 1. The effect of the concentration of the inhibitor on the rate of polymerization of styrene initiated by AIBN at 60°C. [Styrene] = 0.8 M; [AIBN] = 0.001 M; [Inhibitor] = 0.0001–0.001 M. (●) DCP; (○) BPO; (□) KPS; (△) K₂S₂O₈.

Figure 1. The effect of the concentration of the inhibitor on the rate of polymerization of styrene initiated by AIBN at 60°C. [Styrene] = 0.8 M; [AIBN] = 0.001 M; [Inhibitor] = 0.0001–0.001 M. (●) DCP; (○) BPO; (□) KPS; (△) K₂S₂O₈.

FIGURE 104

GTGGGATTATTGAGTGCAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAGTAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTCAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGGCCATTGCAGCTATAACAGCATTAGCACAACACTCGCTCCAA
 TGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG
 TGATTCCTCGAAAAGCATCAGATACAAAATTGTCAATTTTGACCTTAACTTTTGAAGGAA
 AAGTAAAGGAGGATCCTGACCAGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCTGGTTCCTCAGCGCAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTACGCCTCTACTAAAGTTGTATCCGTGGAGCAGGAAACCAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAAGGAAAGAATTGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTGTGCAAACTGACGGAATGGAACGACAGAATATAACTA
 ACCAATCGAAAAATGGATGAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCTTGGCT
 GGTAGCATCACAACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
 TATGTGGAATGTCCGCCACCTTGGTTCCAGTGTGGAAGGATATTACCTCAGTTTGTAA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCAGACCCCAACAGGCAAATTCACCTTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAGTGAACAGAAATTTGAACGTGAAGCAAGCATTTCTCAG
 GAAGTCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGAAAAAGATGTGTGCTAGCTAGGTAAGATGACAACTGCCTGTCTGGCAGTC
 AGCTTCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTCTTCTT
 ACTACAATGCTGAATGACTGGAAGAAGAACTGATATGGCTAGTTACAGTACGTGGTACAGA
 TAATTCAAACCTGCTGTGGTTTTAATTTTGTAACTGTGGCTGATCTGTAATAAAACCTT
 ACATTTTTT

$$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$$
$$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$$

FIGURE 106

TGGTTTTTGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGCCAT
TGCAGCTATAAACAGCATTAGCACAACACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCATAAATTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCG
CAAAGAAGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTAGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGTGCGGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
 GAGTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTCGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGCGGCGAGCCTTTGAGGGGAACGACT
 TGTGCGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC
 CATAACTTCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATTGAGAAATGTAG
 GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGCCATTGCAGCTATAA
 ACAGCATTCAGCACAACTCGCTCCAATGTGATTTTCTACATGTACTCTCAACAATACA
 GCAGACCATCTCCGGTCTCGGGCTCAACAGTGATTCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCTAACTTTTGGAAGGAAAAGTAAAGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCAGCGCAAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTGCCCTTTACAAACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAAGAGATTGTGATTGAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTTGTTGCAAAAC
 CTGACGGAATGGAACGACAGAATATAACTAACCAACTGGAATAATGGATGAAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAAACCTCCTCTGCTTATCG
 TATTTTATCAACGACTCTTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT
 GCTGGAACGATATTACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATTCCA
 GACCAACAGGCAAATTCACCTAATCCGAAGATATACCGAGATCTCAAACATAAGTGAA
 CAGAATTTGAACTGTAAGCAAGCATTTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAATAAGATGTGTGAGCTAG
 GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTTCCTTACTACAATGCTGAATGACTGGAAGAAGAA
 CTGATATGGCTAGTTGAGCTAGCTGGTACAGATAAATCAAACTGCTGTTGGTTTTAATTTT
 GTAACCTGTGGCCTGATCTGTAATAAACTTACATTTTCAATAGGTAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGCCCATAACCAGAGTCTGCGCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGTCTGCTGTCATGGGGGCAGCCATCTCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCGTCTGAGAAGGCCCCACCACCCAGAACCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACCTAAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCCCTCCCTGGTCTCCCACTGTTTGCTGGATAATAAATGGAACCTATGGCTCTAA
AAAAAAAAAAAAAAAAA

FIGURE 109

MGAAISQGALIAIVCNGLVGFLLLLLWVILCWACHSRLPTLTSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGPWPSLEPRT

FIGURE 110

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCTTATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCCTAAGTGGAA
 TCATGTCGGAAGAGATACAATCCTTGCCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
 ATGATGTTTACCTTCAGATTTCATCACCACCCTTCTGGTTCACATTTTCATTTCATTGGTTAT
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTTGTATCGTA
 TCCACAGGCATCAGGCAGTGCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATT
 GACAGTTGAGCTTTTCCAAATCACAAATAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTCTGGGTCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAACCTGCAGGAGCTGCCCAGGTTATGGAAGCGGCCAAGTGAATATAAGCCCT
 TTCGGGCATTCCGTACATGTGGTTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA
 TCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAGTGTTTACTTGTATTTCACAGAAGT
 AAAAAATGATCCTCCTGATCATCCATCCTTTCTGCTCTCTCCATTCTCTCTTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTAACTCTCTGTGGTGAGGATTCCGAGAATCATTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAACCTGCTATTAAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCT
 TGTCCTAAGAACTCAAGTCACTTTACATCTATTAACTGCTTTGGAGACTTCATAATTTTCTA
 GGAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGGCCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAACCTGTGCTGGATGCACCTTTTCTGTGTTTTGCTGTTGAT
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGA
 ATGAGGAGGGAACAGAATCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCT
 GGAACCATTTCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCCTAGAGAAAAGTT
 AGTGAATTTTTTTTTTAAAGACCTAATAAACCTTATCTTCTCTCAAA

FIGURE 111

MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYTNDL
SIELDTERENMKCVLGFAlVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAEQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

FIGURE 112

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC
PAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL
SLPRWRESFIVLESKPKKGVTYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQ
RQDPSGAAAFQKPVGADVSLGLVPKEELSTQSLPEVSLGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATFNKLTHTNSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTQLVLRVCDTDRLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTRIGAVQYTYEQRLEFGFDKYSSKPD
LNAIKRVGYWGGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRIFAMAAHLKG
VITYAIGVAWAAQEELEVIATHPARDHSFVDEFDNLHQYVPRIIQNICTEFNSQPRN

FIGURE 114

CAGGATGAAGTGGTTGCAGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCT**A**
TGCCTTTCCGGCTGCTCATCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT
 GCGCCAGGTCCCGACGGCTCCGCGCCAGATCCCGCCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCAGCTGGACACCTTGCTGATTTGGGGAATGTCTCAGAATCCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGCCGAAAACTCC
 TCCCAGCCTTTAGACCCCCACTGGCATGCCATATGGAACAGTGAACCTACTTCATGGCGTG
 AACCCAGGAGAGACCCCTGTCACTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCTGAGCAGCCTCACTGGTGACCCGGTGTTGAAGATGTGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTGGCAACCAATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGCAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
 GAAAGGAGCCATCTGTCTCAGGATAAGAAAGCTCATGGCCATGTTCTAGAGTATAACAAAG
 CCATCCGGAATACACCCGCTTCGATGACTGGTACCTGTGGGTTAGATGTACAAGGGGACT
 GTGTCCATGCCAGTCTTCCAGTCCCTGGAGGCCACTGGCCTGGTCTTCAGAGCCTCATTGG
 AGACATTGACAATGCCATGAGGACCTTCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGAATTCTACAACATTCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTCCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACTT
 CTTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGGCGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCCTG
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACAATGG
 GTCCAACCTTCGACGCGGTGATACCCCTATGGGGAGTGCATCCTGGGGGCTGGGGGTACA
 TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGTGGAGGACTTGATGAGGAATTCTACTCTCTCAACCGGAGCAGGTC
 GAAATTTAGAAAAACACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAAGTCCCA
 CTTCTCAGCTGCCCCAGTCAGCCCTTCACTCCAAAGTGGCATTACTGGGACAGGTTTTCTT
 AGACTCCTCA**TAA**CCACTGGATAATTTTTTTATTTTTATTTTTTTGAGGCTAAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLMAEEAARKL
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYTVVKQFG
GLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPPTLELGRDAVESIEKISKVECG
FATIKDLRDHKLDRMESFFLAETVKYLYLLFDPTNFIHNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

FIGURE 116

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCCTGGAGA
 AACAGTGTACTATTCTGTGAATAACAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCAGCAGCTGGTGCTCACTCACTGAAGTCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG
 GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGA
 CATTCGTGAAGGCCATTTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTTCCCTGGTACTGGCCCTGTTTGCCCTTTGTTGGCTTCATGCTGATCCTTGT
 GGTCTGCCACTGTTCTCTGGAATAAGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG
 TGGTCTCCAGACACCTTGAAAAAACAATTCACCCAGAAAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCCGTGTCACGGCTGTGATGTCTCTGAGGAACCTCCTCAGGACCTGGAT
 CTCAT**TAG**GTTTTCGGAAGGCCCCAGGTGAAGCCGAGAACCTGTTCTGCATGACATGGAACCC
 ATGAGGGGACAAGTTGTGTTTCTGTTTTCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
 TGAAGTGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC
 CTGGGAAAAGTGAAGTTCATCCCTTCGGTCTTAAGTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTCAG
 TGTTCCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGAGAGAGCCACTTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTGAGTTCACTTCAAGCCCAATGCCGGTGACAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTACAGCCACACTGAAATGGGATGTGCATGAACACGGAGGATC
 CATGAAGTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTGTTGTGCTCCTTTTTTC
 TGTGGTAAAGTACAGAATTCAGCAATAAAAAAGGCCACCCTGGCCAAAAGCGGTAAAAAA
 AAAAAAAAAA

FIGURE 117

MQFTTMVLEEIWTSLFMWFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAIGE
 TVVYSVEYQGEYESLYTSHIWIPISSWCSLTEGPECVDITATVPYNLRVRATLGSQTS
 SILKHPFNRRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
 GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVQGEAIPLVLALFAFVGFMILIV
 VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGAGGGGCGAACCCTTGC GGCGCAAGGG
GTTNGCGAACCCTTGGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCGGCCACCTCCGGAACAAGCC**ATG**GTGGCGGCGACGGTGGCAGCGGCGGTG
GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
TCAACATCCGGGGCAAACCTGGTGTGCTGCGTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
AATGTGGCCAGCGAGTGC GGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
AGACCTGGGCCCCCACCACCTTTAACGTGCTCGCCTTCCCTTGAACCAAGTTTGGCCAACAGG
AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGCACCTACAGTGTCTCATTCCCC
ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGGCCATCCTGCCTTCAAGTACCTGGCCCA
GACTTCTGGGAAGGAGCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGG
TGGTAGGGGCTTGGGACCCAACTGTGTGAGTGGAGGAGTGCAGACCCAGATCACAGCGCTC
GTGAGGAAGCTCATCTACTGAAGCGAGAAGACTTA**TAA**CCACCGCGTCTCCTCCTCCACCA
CCTCATCCCGCCACCTGTGTGGGGCTGACCAATGCAAACTCAAATGGTGTCTCAAAGGGAG
AGACCCACTGACTCTCCTTCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA
AAATTCTAGTATTTTGATTATTGTAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAG
AGCTCTTGACCAAGTGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAA
TAGAAGTATATCAAGCAATAATCTCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTAC
CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
CAAATAGGAGGCATTCAATGAACATTTTTTGTCATATAAACCAAAAAATAACTTGTATCAAT
AAAAACTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
GTATTTCCTCTGTATTATTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA
ACAATACCTCACGATATAAAATAAAAAATGAAAGTATCCTCCTCAAAAA

MVAATVAAAWLLWAAACAQQEQDFYDFKAVNIRGKLVSLKEYRGVSVLVNVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFCPNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSGKEPTWNFWKYLVA PDGKVVGAWDPTVSVEEVRPQITALVRKLLIKREDL

1. $\frac{1}{2}$ 2. $\frac{1}{3}$ 3. $\frac{1}{4}$ 4. $\frac{1}{5}$ 5. $\frac{1}{6}$ 6. $\frac{1}{7}$ 7. $\frac{1}{8}$ 8. $\frac{1}{9}$ 9. $\frac{1}{10}$ 10. $\frac{1}{11}$ 11. $\frac{1}{12}$ 12. $\frac{1}{13}$ 13. $\frac{1}{14}$ 14. $\frac{1}{15}$ 15. $\frac{1}{16}$ 16. $\frac{1}{17}$ 17. $\frac{1}{18}$ 18. $\frac{1}{19}$ 19. $\frac{1}{20}$ 20. $\frac{1}{21}$ 21. $\frac{1}{22}$ 22. $\frac{1}{23}$ 23. $\frac{1}{24}$ 24. $\frac{1}{25}$ 25. $\frac{1}{26}$ 26. $\frac{1}{27}$ 27. $\frac{1}{28}$ 28. $\frac{1}{29}$ 29. $\frac{1}{30}$ 30. $\frac{1}{31}$ 31. $\frac{1}{32}$ 32. $\frac{1}{33}$ 33. $\frac{1}{34}$ 34. $\frac{1}{35}$ 35. $\frac{1}{36}$ 36. $\frac{1}{37}$ 37. $\frac{1}{38}$ 38. $\frac{1}{39}$ 39. $\frac{1}{40}$ 40. $\frac{1}{41}$ 41. $\frac{1}{42}$ 42. $\frac{1}{43}$ 43. $\frac{1}{44}$ 44. $\frac{1}{45}$ 45. $\frac{1}{46}$ 46. $\frac{1}{47}$ 47. $\frac{1}{48}$ 48. $\frac{1}{49}$ 49. $\frac{1}{50}$ 50. $\frac{1}{51}$ 51. $\frac{1}{52}$ 52. $\frac{1}{53}$ 53. $\frac{1}{54}$ 54. $\frac{1}{55}$ 55. $\frac{1}{56}$ 56. $\frac{1}{57}$ 57. $\frac{1}{58}$ 58. $\frac{1}{59}$ 59. $\frac{1}{60}$ 60. $\frac{1}{61}$ 61. $\frac{1}{62}$ 62. $\frac{1}{63}$ 63. $\frac{1}{64}$ 64. $\frac{1}{65}$ 65. $\frac{1}{66}$ 66. $\frac{1}{67}$ 67. $\frac{1}{68}$ 68. $\frac{1}{69}$ 69. $\frac{1}{70}$ 70. $\frac{1}{71}$ 71. $\frac{1}{72}$ 72. $\frac{1}{73}$ 73. $\frac{1}{74}$ 74. $\frac{1}{75}$ 75. $\frac{1}{76}$ 76. $\frac{1}{77}$ 77. $\frac{1}{78}$ 78. $\frac{1}{79}$ 79. $\frac{1}{80}$ 80. $\frac{1}{81}$ 81. $\frac{1}{82}$ 82. $\frac{1}{83}$ 83. $\frac{1}{84}$ 84. $\frac{1}{85}$ 85. $\frac{1}{86}$ 86. $\frac{1}{87}$ 87. $\frac{1}{88}$ 88. $\frac{1}{89}$ 89. $\frac{1}{90}$ 90. $\frac{1}{91}$ 91. $\frac{1}{92}$ 92. $\frac{1}{93}$ 93. $\frac{1}{94}$ 94. $\frac{1}{95}$ 95. $\frac{1}{96}$ 96. $\frac{1}{97}$ 97. $\frac{1}{98}$ 98. $\frac{1}{99}$ 99. $\frac{1}{100}$ 100. $\frac{1}{101}$ 101. $\frac{1}{102}$ 102. $\frac{1}{103}$ 103. $\frac{1}{104}$ 104. $\frac{1}{105}$ 105. $\frac{1}{106}$ 106. $\frac{1}{107}$ 107. $\frac{1}{108}$ 108. $\frac{1}{109}$ 109. $\frac{1}{110}$ 110. $\frac{1}{111}$ 111. $\frac{1}{112}$ 112. $\frac{1}{113}$ 113. $\frac{1}{114}$ 114. $\frac{1}{115}$ 115. $\frac{1}{116}$ 116. $\frac{1}{117}$ 117. $\frac{1}{118}$ 118. $\frac{1}{119}$ 119. $\frac{1}{120}$ 120. $\frac{1}{121}$ 121. $\frac{1}{122}$ 122. $\frac{1}{123}$ 123. $\frac{1}{124}$ 124. $\frac{1}{125}$ 125. $\frac{1}{126}$ 126. $\frac{1}{127}$ 127. $\frac{1}{128}$ 128. $\frac{1}{129}$ 129. $\frac{1}{130}$ 130. $\frac{1}{131}$ 131. $\frac{1}{132}$ 132. $\frac{1}{133}$ 133. $\frac{1}{134}$ 134. $\frac{1}{135}$ 135. $\frac{1}{136}$ 136. $\frac{1}{137}$ 137. $\frac{1}{138}$ 138. $\frac{1}{139}$ 139. $\frac{1}{140}$ 140. $\frac{1}{141}$ 141. $\frac{1}{142}$ 142. $\frac{1}{143}$ 143. $\frac{1}{144}$ 144. $\frac{1}{145}$ 145. $\frac{1}{146}$ 146. $\frac{1}{147}$ 147. $\frac{1}{148}$ 148. $\frac{1}{149}$ 149. $\frac{1}{150}$ 150. $\frac{1}{151}$ 151. $\frac{1}{152}$ 152. $\frac{1}{153}$ 153. $\frac{1}{154}$ 154. $\frac{1}{155}$ 155. $\frac{1}{156}$ 156. $\frac{1}{157}$ 157. $\frac{1}{158}$ 158. $\frac{1}{159}$ 159. $\frac{1}{160}$ 160. $\frac{1}{161}$ 161. $\frac{1}{162}$ 162. $\frac{1}{163}$ 163. $\frac{1}{164}$ 164. $\frac{1}{165}$ 165. $\frac{1}{166}$ 166. $\frac{1}{167}$ 167. $\frac{1}{168}$ 168. $\frac{1}{169}$ 169. $\frac{1}{170}$ 170. $\frac{1}{171}$ 171. $\frac{1}{172}$ 172. $\frac{1}{173}$ 173. $\frac{1}{174}$ 174. $\frac{1}{175}$ 175. $\frac{1}{176}$ 176. $\frac{1}{177}$ 177. $\frac{1}{178}$ 178. $\frac{1}{179}$ 179. $\frac{1}{180}$ 180. $\frac{1}{181}$ 181. $\frac{1}{182}$ 182. $\frac{1}{183}$ 183. $\frac{1}{184}$ 184. $\frac{1}{185}$ 185. $\frac{1}{186}$ 186. $\frac{1}{187}$ 187. $\frac{1}{188}$ 188. $\frac{1}{189}$ 189. $\frac{1}{190}$ 190. $\frac{1}{191}$ 191. $\frac{1}{192}$ 192. $\frac{1}{193}$ 193. $\frac{1}{194}$ 194. $\frac{1}{195}$ 195. $\frac{1}{196}$ 196. $\frac{1}{197}$ 197. $\frac{1}{198}$ 198. $\frac{1}{199}$ 199. $\frac{1}{200}$ 200. $\frac{1}{201}$ 201. $\frac{1}{202}$ 202. $\frac{1}{203}$ 203. $\frac{1}{204}$ 204. $\frac{1}{205}$ 205. $\frac{1}{206}$ 206. $\frac{1}{207}$ 207. $\frac{1}{208}$ 208. $\frac{1}{209}$ 209. $\frac{1}{210}$ 210. $\frac{1}{211}$ 211. $\frac{1}{212}$ 212. $\frac{1}{213}$ 213. $\frac{1}{214}$ 214. $\frac{1}{215}$ 215. $\frac{1}{216}$ 216. $\frac{1}{217}$ 217. $\frac{1}{218}$ 218. $\frac{1}{219}$ 219. $\frac{1}{220}$ 220. $\frac{1}{221}$ 221. $\frac{1}{222}$ 222. $\frac{1}{223}$ 223. $\frac{1}{224}$ 224. $\frac{1}{225}$ 225. $\frac{1}{226}$ 226. $\frac{1}{227}$ 227. $\frac{1}{228}$ 228. $\frac{1}{229}$ 229. $\frac{1}{230}$ 230. $\frac{1}{231}$ 231. $\frac{1}{232}$ 232. $\frac{1}{233}$ 233. $\frac{1}{234}$ 234. $\frac{1}{235}$ 235. $\frac{1}{236}$ 236. $\frac{1}{237}$ 237. $\frac{1}{238}$ 238. $\frac{1}{239}$ 239. $\frac{1}{240}$ 240.

FIGURE 121

CGGACGCGTGGGCGGGCGGGACGACGAGGCAAGCGAGCC**ATGG**CTGTCTACGTCGGGATGC
 TGCCTCTGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGTGGGGGCCGGGCGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCTCAGTTCCAGAGAGGTGGATCG
 CATGGTCTCCACGCCCATCGGAGGCCCTCAGCTACGTTACGGGGTGACCAAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCTTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC
 TTGGTCGCTCTCCATGAAGACGTCAGGTTGACCTTTGCCAACTCAAGGAGGAGGTGGACAA
 AGCTGCTTCTGGCCTCCTGAGCATTGGCCTCTGCAAAAGGTGACCGGCTGGGCATGTGGGGAC
 CTAACCTCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCAGGCGGGCATCATTTCTGGTG
 TCTGTGAACCCAGCCTACCAGGCTATGGAAGTGGAGTAIGTCTCAAGAAGGTGGGCTGCAA
 GGCCTTTGTGTTCCCAAGCAATTCAGAGCCAGCAACTACAACGTCCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGGCTTGAAGAGTCAGAGGCTCCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTTGGCGGGGACCCTGCTCCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACCAGCAGTTCTGTCTGCCATG
 ACCCATCAACATCCAGTTACCTCGGGGACAAAGGCGAGCCCCAAGGGGGCCACCTCTCC
 CACTACAACATTGTCAACAACTCCAACATTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCTGCCAACCCCCGTACCATTGCCTGGGTTCGTGGCAG
 GCACAATGATGTGTCTGATGTACGGTGCCACCCTCATCTGGCCTCTCCCATCTTCAATGGC
 AAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGCACTTCTGTATGGTACCCCCACGAT
 GTTCGTGGACATTTGAACCCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTGTCAATTGCTGGGTCCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 ATGAAGGACCTGGTGGTTGCTTATGGAACCACAGAGAAGCTCCCGTGACATTCGCGCACTT
 CCTGTAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATATGCCTCACACGGAGG
 CCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAAGCTGAACACGCCCCGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTGCCACAATGAATGAGCAGGCTTCTGCA
 AGATCGTGGGCGCTCTAAGGATATGATCATCCGGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTCACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA
 CGATCGATGGGGGAAGAGATTGTGCCTGCATTGCGCTGAAGGACGGGGAGGAGACCACGG
 TGGAGGAGATAAAAGCTTTCTGCAAAAGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
 GTGTTTGTCAAACTACCCCTCACCATTTTCAGGAAGATCCAGAAATTCAACTTCGAGA
 GCAGATGGAACGACATCTAAATCTG**TGA**ATAAAGCAGCAGGCTGTCTGGCCGGTTGGCTT
 GACTCTCTCTGTGAGAATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGCAGCCAGTTT
 TGAGCCAGGACATCAAATGTCAAGGAATTGACTGAACGAACTAAGAGCTTCTGGTGGGT
 CGGGAACTCGCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCCTG
 TCCATCCCCACATTCCTCGTGTGCTTGTGATTTGGCATAAAGAGCTTCTGTCTTTCTTT
 GAAAAAAAAAAAAAAAAA

FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRWQEARLQGVRFLLSSREVDRMVSTPIGGLSYVQ
 GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
 DRLGMWGFNSYAWVLMLQATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
 YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGTLLLDDEVVAAGSTRQHLDQLQYN
 QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSAVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPVTFAHFPEDTVEQKAESVG
 RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT
 MNEQGFCIKIVGRSKDMIIRGENIYPAELEDFHHPKVQEVQVVGKDDRMGEEICACIRL
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATTCGCTGGGTTCGTTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCTCATCCTGGCCTCTCCATCTTCAATGGCAAGAAGGCACCTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAATATGAAGGACCTGGTGGT
TGCTTATGGAACACAGAGAACAGTCCCGTGACATTTCGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTGCGCCAC

FIGURE 124

GAGCAGGACGGAGCC**ATG**GACCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTTCCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGGG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
 AGTGCGGGGTTGCGGTTGCGGACTCCCCGGCAAGAATGACCGCGGCTGGATCTTACGGGC
 TTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCGCCCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCGCCGGTCTGTAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCAGCGGCAACGTACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACCTCGGGA
 TGGAGTAACAGGGCCAGGGTTACGCTCAGTGGCTCCTGTGTGCCAGGGGTCCCGCTGTAACCT
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCCACCCCTTGTCCGGCTGCCCCCT
 CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG
 ACCCACATCCACCACCAAAACCATGCCAGCGCCAACCAGTCAAGTCCGAGACAGGGAGTAG
 AACACGAGGGCTCCCGGATGAGGAGGCCAGGTTGACTGGAGGCGCCGTGGCCACCAGGAC
 CGCAGCAATTACAGGCAGTATCCTGCAAAAGGGGGGCCAGCAGCCCCATAATAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTG**T**
GAGCTTCTCCACCTGGAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATCACTTCTGTTCACCACCTGGACTGGCTGGGCTGGCCAGCCCCGTGTTTTCCAACATTCGC
 CAGTATCCCCAGCTTCTGTGCGCTGGTTTGGCGCTTTGGGAAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC
 TCCGCTTGTCTTCTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACAGGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCCTACTACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
 GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCCTACTCCCCGATCTTTGGG
 GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTAC
 CCAATTCGCCCTATAGTGAGTCGTA

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCS PNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGLPGKNDRGLDLHGLLAFIQLQQCAQDRCAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPFVVCYNASDHVYKGCDFGNVTLTAANVTV
SLPVRGCVQDEFCTRDGVTGPGFTLSGCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT
VASTTSVTTSTSAPVRPTSTTKPMPAPTSQTPRQGEHEASRDEEPRLTGGAAGHQRDSNSG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

[illegible][illegible]

FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDDEEAQVENLITANATEPQKQRTVEVQPSGGSGLWNLRRLLEPLDANVDA

[illegible]

FIGURE 128

AAACTTGACGCCATGAAAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCTTGAAGTGGCAGCCCTCTTTGAGTCTATCAAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCTTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTCCTGCCTCAGGAACTCCAATAAAACATTTCCATCCAAA

FIGURE 129

MKIPVLPVVLSSLVLVLSAQGATLGGPEEESTIENYASRPEAFNTFFLNIDKLRSFAKADE
FLNWHALFESIKRKLPFLNWDAFPKLKGLRSATPDAQ

$\frac{d^2x}{dt^2}$
 $\frac{d^2y}{dt^2}$
 $\frac{d^2z}{dt^2}$
 $\frac{d^2t}{dt^2}$
 $\frac{d^2x}{dt^2}$
 $\frac{d^2y}{dt^2}$
 $\frac{d^2z}{dt^2}$
 $\frac{d^2t}{dt^2}$
 $\frac{d^2x}{dt^2}$
 $\frac{d^2y}{dt^2}$
 $\frac{d^2z}{dt^2}$
 $\frac{d^2t}{dt^2}$
 $\frac{d^2x}{dt^2}$
 $\frac{d^2y}{dt^2}$
 $\frac{d^2z}{dt^2}$
 $\frac{d^2t}{dt^2}$
 $\frac{d^2x}{dt^2}$
 $\frac{d^2y}{dt^2}$
 $\frac{d^2z}{dt^2}$
 $\frac{d^2t}{dt^2}$

FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCC**ATG**GGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTT
TTCTCCAGCCAGTTCCAACTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTC**ATGA**GAGTGTTCCTTTGTGTAAAGTATTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCCTCA
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTAAGGTCCCTTTATTTTT
AGGTTCAAGGTTTCATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATC
TTCATATTAATTGTAACGATTAATAAGAGCAGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTGAGTATATTTTCACTAGATATTTGTATAGAAAGACTGAATAGTGATG

MGVEIAFASVILTCLSLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

$$f_{\text{max}} = \frac{1}{2\pi} \sqrt{\frac{1}{L C_{\text{eff}}}} = \frac{1}{2\pi} \sqrt{\frac{1}{L (C_1 + C_2)}}$$

FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGCGC**ATG**AGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCTCTCCTGCCCTCAGCGCAGGGCCGCCAGAGGAGTCAGGTTCAAATGGA
 AAGTATTTATTGACCAAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
 TGCAGCTGCTACCATGGTGTCTAGAAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGGAATAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCTCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGACCTGCTGTTTGGCCAATTTAT
 CCTACAGGTCTTGGACGTTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG
 GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAGTCCAGAACGAG
 ATCCTCTCATTCTTCTGTCTCGGAAAAACCCAAACTTGTTGATGCAGAATACACCAAAAAC
 CAGGCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAATACAAGTATCTGTTTAAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTTCTGTGTGGCTCACTGTGTTTCCATGTTGGTGATGAGTGGCTAGAATCTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
 TCCCAAAATGTTGAAAACCTGAAGT**TAG**TAGTCATCATAGGACCATAGTCCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTTCAATTTCTTAAGACCAATC
 ACAGCTTGTGCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCCATTATTTGGAGCAGAAAATTGTCATTTGGAAGTAGTACAA
 CTCATTGCTGGAATTGTGAAATTATTCAAGGCGTGATCTCTGTCACTTTATTTTAAATGTAGG
 AAACCCCTATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTCTCTTTTGTAACCATAAACTCTGTTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTCTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLLFLLLPSAQGRQKESGSKWKVFIDQINRSLENYEPCSSQNCSCYHGVIE
 EDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPD
 MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPVWPIYPTGLGRWDL
 FREDLVRSAAQWPWKKNSTAYFRGSRTSPERDPLILLSRKNPKLVD AEYTKNQAWKSMKDT
 LGKPAAKDVHLVDHCKYKYLENFRGVAASFRFKHLFLCGSLVFHVGD EWELEFFYPQLKPWVH
 YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSY
 NVTRRKG YDQIIPKMLKTEL

FIGURE 134

CACCCCTCCATTCTCTGCCATGGCCCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCTGGCCTTTGGCACCGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTTGTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGTACTTTGGGGTCCCTCAG
 AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTTGCACTGGTGATGCGGTACTGGGAGCC
 CATAACCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCG
 TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
 TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCCACCTGCCCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGTGTGGGTGGTGCTACCCTGGGCACGGACCGTCTCCTCCTTGCT
 TTCCTCCTTACCCTCTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
 CCGGGCCACAGTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAGT
GAGGAGGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCTCCCACTGAATTCTAAATCCTTAAC
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCCCTAAATCTGAGTTTCAGCCA
 CTGAATCCAAGGTCCACTTCTACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCCTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACTCCCCTGGCACTGTTACTTGCTCTGCGCCTCAGGGGTCCCCCTTCTGCACCGCT
 GGCTTCCACTCCAAGAAGGTGGACCAGGCTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA
 GGCCCCAACCTTGCTCACCCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGATTCTCCTGCTCTTAAGTTCGATGACTTGGGGCTC
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAGTCAGCCTTTTCTAAAAAAA

FIGURE 135

MAPALLLI PAALASFILAFGTGVEFVRF TSLRPLLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFVGQHS LMAAERVKAWTSRYFGVLQRS LYVACTALALQLVMRYWEP I PKGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDY AELMGLKQVYYHVLGLGEPLALKSP
RALRLFSHLRHFPVCVELLTVLWVPTLGTDRLLLAFL LTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGT
 TTTAATTAAGCATGGAATACAGAAAAACAACAAAACTTAAGCTTTAATTCATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGCTCTCCGACTACTACCCCCGAGTGTAAGAACCTTCGGCTCGCGTGCTTCTG
 AGCTGCTGTGGC**ATG**GCGCTCGGCTCTCTGGACTGTCCTTCCGAGTAGGATGCTACTGAGATCC
 CTCAAATGGAGCCTCCTGCTGCTGCTACTCCTGAGTTCCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAAGCGGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACCTTCACACTTCGAGAGCATTCAAACGTCTCTATCAAAATCCATTT
 CTGGTCATTCTGGTGACCTCCACCCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTGAAAACCATTTATGGC
 ATTCAGGTGGGTAAGTGTGTTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTTATCCTCTAATTGATAATATTCCCTATAGAGGATTTTACCAAAAAACCATAT
 TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTTATATAA
 TGTCAGAGATTTGGTGCCAAAGGATCTATGAAATGATGGGTCACGTAAAACCATCAAGTTT
 GAAGATGTTTATGTGCGGATCTGTTTGAATTTATTAAGTGAACATTCAATTTCCAGAAGA
 CACAAATCTTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTTGGCAGGTCATGCTAAGGAACACC
 ACATGCCATTAT**TAA**CTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
 GTGTAAATAAAGTAGGTACTGTGGAAAATTTCATGGGGAGGTGAGTGTGCTGGCTTACACTG
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGCTAAA
 GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG
 TGTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACAATGTAGAGTTTATTATTATG
 AACATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAAGTACTTCAAGATGTTGACGATTTCAATACAAGATAAAAGGATAGTGAAT
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAGGATAGTGAAT
 CATTCTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC
 TCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTTGTAAAT
 ATTTTACTGTGTAATATAGAGAAGAATTAAAGCAAGAAAATCTGAATA

FIGURE 137

Parameter	Value	Unit
μ_0	0.001	mm
μ_1	0.001	mm
μ_2	0.001	mm
μ_3	0.001	mm
μ_4	0.001	mm
μ_5	0.001	mm
μ_6	0.001	mm
μ_7	0.001	mm
μ_8	0.001	mm
μ_9	0.001	mm
μ_{10}	0.001	mm
μ_{11}	0.001	mm
μ_{12}	0.001	mm
μ_{13}	0.001	mm
μ_{14}	0.001	mm
μ_{15}	0.001	mm
μ_{16}	0.001	mm
μ_{17}	0.001	mm
μ_{18}	0.001	mm
μ_{19}	0.001	mm
μ_{20}	0.001	mm
μ_{21}	0.001	mm
μ_{22}	0.001	mm
μ_{23}	0.001	mm
μ_{24}	0.001	mm
μ_{25}	0.001	mm
μ_{26}	0.001	mm
μ_{27}	0.001	mm
μ_{28}	0.001	mm
μ_{29}	0.001	mm
μ_{30}	0.001	mm
μ_{31}	0.001	mm
μ_{32}	0.001	mm
μ_{33}	0.001	mm
μ_{34}	0.001	mm
μ_{35}	0.001	mm
μ_{36}	0.001	mm
μ_{37}	0.001	mm
μ_{38}	0.001	mm
μ_{39}	0.001	mm
μ_{40}	0.001	mm
μ_{41}	0.001	mm
μ_{42}	0.001	mm
μ_{43}	0.001	mm
μ_{44}	0.001	mm
μ_{45}	0.001	mm
μ_{46}	0.001	mm
μ_{47}	0.001	mm
μ_{48}	0.001	mm
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μ_{67}	0.001	mm
μ_{68}	0.001	mm
μ_{69}	0.001	mm
μ_{70}	0.001	mm
μ_{71}	0.001	mm
μ_{72}	0.001	mm
μ_{73}	0.001	mm
μ_{74}	0.001	mm
μ_{75}	0.001	mm
μ_{76}	0.001	mm
μ_{77}	0.001	mm
μ_{78}	0.001	mm
μ_{79}	0.001	mm
μ_{80}	0.001	mm
μ_{81}	0.001	mm
μ_{82}	0.001	mm
μ_{83}	0.001	mm
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μ_{92}	0.001	mm
μ_{93}	0.001	mm
μ_{94}	0.001	mm
μ_{95}	0.001	mm
μ_{96}	0.001	mm
μ_{97}	0.001	mm
μ_{98}	0.001	mm
μ_{99}	0.001	mm

FIGURE 138

CCTCTGTCCACTGCTTTCGTGAAGACAAGATGAAGTTTACAATTGTCTTTGCTGGACTTCTT
 GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
 TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
 ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
 AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
 TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
 CTCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
 AAAAACATTGCAAACATGTGTCTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
 AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
 CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
 CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
 TTTCTCTACTAGTTATGTTGATTTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDNNDNNAGSGQQSVSVNNEHNVANVDNNGWDSWNS
 IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQGKPGGPPPKGLMYSVN
 PNKVDDLKFKGNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

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FIGURE 140

CATTCTGAACTAATCGTGTGAGAAATGACTTTGAAAGCATGTCTTTTACAGAAGTATA
 TTAACCTTTTAGGAGTAATTTCTAGTTGGATTGTAATATGAAATAATTTAAAGGGCTTCG
 CTCATATATAGGAAAAATCGCATATGGTCCCTAGTATTAATTCCTATTGCTTACTGATTTTTT
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGTGGTTTGTTCATG
 CAAGCTTATAGTTGAAATATTTTTTCAGGAATTAC**ATGA**ATGACAGTCTTCGAACCAATGTGT
 TTGTTTCGATTTCACCCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
 CAGATTCGGTTGCCAACTCGTCCCATTTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACGAAAAAAGCCAAACTATGAATTAC
 TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA
 TTGAATCCGGATGGAAGTCCAGCCCTTCAACCTGGGTGGATTTTCTCCAGCCTCCAAGCC
 ATCATCACCAAGAGAAGTAAAGCTGAAGAGAAATCACCAATCTCCATTATGTGAAGACAG
 TCAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTGAAGAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
 GGTCTCTCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
 TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGATCACTCAGATGCAG
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
 GAGAGGTCCCATAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTTCTCTCTCTTTGAGCCTGCATCAGTTCTTGGTTTTGCCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAAACATTAACGCAAACTGATTAGGATTTGATTTCTTGAACCCCTCTA
 GGTCTCTAGAACACTGAGGACAGTTTCTTTGAAAAGAACTATGTTAATTTTTTGCACATT
 AAAATGCCCTAGCAGTATCTAATTAATAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
 TGTGTATTGTTTATTGCTATAAGAAGTGGAGCGTGAATCTGTAAAAATGTATCTTATTTTT
 ATACAGATAAAATTGCAGACACTGTTCTATTTAAGTGGTTATTGTTTAAATGATGGTGAAT
 ACTTCTTAACACTGGTTTGTCTGCATGTGTAAGATTTTTTACAGGAAATAAAATACAAAT
 CTGTTTTTTTCTAAAAAAGT

FIGURE 141

MNDSLRTNVFVRFQPETIACACIYLAARALQIPLPTRPHWFLFLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYN
NRRSRSGTYSSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKKRSRSRQ
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKSKHHGGSRSRSGHGRHR

FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAGATTATTGGAAGGGGTTTATCA
 TTTTTTGAANNATTTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTTACAGAAATATAT
 TANCITTTTAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
 CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATNTTTATTGCTTACTGATTTTTTTG
 AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAAGA
 ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTTGTTTACATGCA
 AGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
 GTTCGATTTCACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
 GATCCGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAATCC
 AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG
 GAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAAAGCAAAGGGATT
 GAATCCGGATGGAAGCTCCAGCCCTTCAACCCCTGGGTGGATTTTCTCC

FIGURE 143

GGCACGAGGCCTCGTGCCAAGCTTGGCACGAGGGTGACCCGCTTCTCGCACGCGTCATGGC
 GGTCTCGGAGTACAGCTGGTGGTGACCTGCTCACTGCCACCTCATGCACAGGCTGGCGC
 CACACTGCTCCTTCGCGCGCTGGCTGCTGTGAACGGCAGTTTGTTCGATACAAGCACCCG
 TCTGAGGAGGAGCTTCGGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
 GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCCAGCTGG
 AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCTCGGAGTACCACTGTT
 TTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTTACAGAGGCCACTACTACAT
 GCTGGGACAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT
 CCATCAAGATGTTCTCTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC
 TCTGTCTGCCTCACCTTTGCTTCTCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG
 GGAGGAGACCCCTCGAGCTGGGGCTGGAGCCTGGTCTGGCCAGCATGACCCAGAAGTTAGAGC
 CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCCTGTGGCCAAAGCTGGCTATCCGCGTG
 GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCCTCACCTTCCAGGCCTGCGGGTGGC
 CCAGACCCACCGGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAAGTTCTCTCTGC
 ACACAGCTTCCTGTCTCCCTGTTCATCCTGTGGCTCTGGACAAAGCCCATTCGACGGGAC
 TTCTTGACACAGCCGCCGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
 CTCTGGGCGCCTCTGTTGCTGGTGGTGTGCTGCTGCTGCGGCTGGCGGTGACCCGGCCCC
 ACCTGCAGGCCTACCTGTGCCTGGCCAAAGCCCGGGTGGAGCAGTGCAGAGGGAGGCTGGC
 CGCATCGAAGCCCGTGAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
 GAGCTTGCAGTACCTGACGCCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC
 TGGGAGGCTATTCCTGGGGCTGGGCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
 AGCGCTGCCCCCATCGGCTCTGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
 GGCCCTGGGTGGCTGCTTACTCCCTCTTCTCCGTGGCGTCTGGGCTACCTCATCTGGT
 GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGCTCTACTTCCACCACTTGGCA
 GGCTCCATAGTGCCTGCAGACCTCCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGGACA
 CTAGCCTGCCCCCTCTGTTTGGCCCCCGTGTCCCCAGCTGCAAGGTGGGGCCGGACTCCCC
 GCGGTTCCCTTCAACACAGTGCCTGACCCGCGGCCCCCTTGGACGCCGAGTTCTGCTCA
 GAACTGTCTCTCTGGGCCCAGCAGCATGAGGGTCCCAGGCCATTGTCTCCGAAGCGTATG
 TGCCAGGTTTGAGTGGCGAGGGTGATGCTGGCTGCTTCTGAACAAATAAAGGAGCATGCC
 GATTTTTAA

FIGURE 144

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
 RWANGLSEEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
 YMLGPAKETNIAVFWCLLTVTFSIKMFLT VTRLYFSAEEGERSVCLTFAFLFLLLAMLVQV
 VREETLELGLEPGLASMTQNLEPLLKKQGWWDALPVAKLAI RVGLAVVGSVLGAFLTFPGLR
 LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQP PFGETRFSLLSDSA
 FDSGRWLWLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
 VVSLQYLTPLILT LNCTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVOQTAARI
 AGALGGLTPLFLRGVLAYLIWWTAAQCQLLASLFGLYFHQHLA GS

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC
 CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTT
 TGTTCGGATACAAGCACCCGTTNTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
 CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
 GAGATGCCCGGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
 TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGGTACCTCTT
 CACAGAGGCCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
 GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGC
 GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTGCCTTCCTCTTCCTGCTGCTGGC
 CATGCTGGTGCAAGCG

FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGGCCGTGATTTATTAAAGTGCCCT
 AATCTGAAGGTTCTCAGTCAAAATCTTTGTGATCTACTGATTGTGGGGGCGATGGCAAGGTTTGCTTTAAAGGAGC
 TTGGCTGGTTTGGGCGCTTGTAGCTGACAGAAGTGGCCAGGGAGAAATGCAGCACATCTGCTCGGAGAAATGAAGG
 CGCTTCTGTTGCTGGTCTTGGCTTGGCTCAGTCTCTGCTAACTACATTGCAAAATGTGGGCAACCTGCACCTCTCTG
 TATTGAGAATCTGTAAAGGTGCTCCCACTACGGCTCACCAGAAATAGGAAGAGCGCTCACCAAGATGGCTG
 TCCAGACGGCTGTGGGAGCTCACAGCCACGGCTCCCTCCCAGAGGTTTCTGCAGCTGCCACCATTCTCCTTAA
 TGCACAGACGAGCTGGGCTTACACAACCTTGCTACGTGTCCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCGAACTAGGGCAGCGCCCTTTGAGAGATCCACTATTAGAGCAGATCATTAA
 AAAAATAAATCGAGCTTTGAGTGTCTTCTCGAAGGACAAAAGCGGGAGTGCAGTTGCCAACCATGCCGACCAGG
 GCAGGGAAAATTTCTGAAAACACCACTGCCCTGAAGTCTTTCCAGGTTGTACCACCTGATCCAGATGGTGAA
 ATTACAGCATCAAGATCAATCGAGTAGATCCCAGTGAAGGCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTATCCAACACATTATCTGTGATGGGGTATCGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCAACAACACGCTGTGCGTCTCTGCGG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAAAGAGTTCGCCAGCAGGAACAATGGACAGGCCCC
 GGATGCTACAGACCCGAGATGACAGCTTTTATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGA
 TAAAATGGTGGCGAAGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTCGATATGGCAGCCAGAAAAG
 TGCGGCTCATCTGATTGAGGCCAGTGAAGACGTGTTCACTCGTGTGTCGCCAGGTTGCGCAGCGGAGCC
 CTGACATCTTTGAGGAAGCCGGCTGGAAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGAGAGGAGCAACACT
 CCCAAGGCCCTCCATCTTACAATTACTTGTGATGAGAAGTGGTAAATATCCAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTGCAGGGGGAGCATCACATAGAGAATGGGATTGGCTATCTATGTGATCAGTGTGAGCCCG
 GAGGAGTCATAAGCAGAGATGGAGAATAAAAACAGGTGACATTTTGTGAATGGATGGGGTCGAATCGACA
 GAGGTGAGCCGAGTGGAGCAGTGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGT
 CAAAGAGTATGAGCCCCAGGAAGATGCAGCAGCCAGCAGCCCTGGACTCCAAGCACACATGGCCCCACCCA
 GTGACTGGTCCCCATCTGGGTGATGTGGCTGGAATTACACGGTGCTGTGTAATCTGAAAGATATTGTATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTCTGCAATTGAGGAGTTATGAAGAAATACAATGGAAGAACAACTTT
 TTTTCATCAATCCATTGTTGAAGGAACACAGCATACAATGATGGAAGATAGATGTGGTGATATTCTTCTTG
 CTGTCATGTTGTAAGTACATCAGGAATGATACATGCTTGCTTGGCAAGACTGTGAAGAACTTAAAGGAAGA
 ATTACTCTAATATTGTTCTTGGCTGGCAGCTTTTTTATAGAAATCAATGATGGGTGAGGAGAAAACAGAAAAA
 TCACAAATAGGCTAAGAAAGTTGAAACATATATTTATCTTGCAGTTTATATTTTAAAGAAAGAAATACATTGT
 AAAAATGTGAGGAAAAGTATGATCATCTAATGAAAGCCAGTTACACCTCAGAAAAATGATTCAAAAAAATTA
 AAATCTAGTATGTTTTTTTTCAGTGTGGAGGATTTCTCATTACTACACAACTTGTATATTTTTTTCATTCAAT
 AAAAAGCCCTAAAAACAACTAAATGATTGATTTGATATCCCACTGAATCAGCTGATTTAAATTTAAATTTT
 GGTATATGCTGAAGCTGCCAAGGGTACATTATGGCCATTTTAAATTACAGCTAAATATTTTTTAAATGCA
 TTGCTGAGAACCGTTGCTTTTCATCAACAGAATAAATATTTTTTCAGAGTTTAA

FIGURE 147

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTAT
APSPFEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISFVDSGRSNRTRARPFERSTIRSR
FKKINRALSVLRRTKSGSAVANHADQGRESENNTAPEVFPRLYHLIPDGEITSIKINRVDP
SESLSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGV
FIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRS
PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPPGGVISRDGRIKTGDILLNVVGVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSVMMWLELPRCLYNCKDIVLRNTAGSLGFCIV
GGYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTGTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCTCTCCAGGCAAAATGGTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCAC
CCATTGAGAACTCTGCAAAACATATCCCTTTGTATAAGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTGATGTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAAGTCAAATTAATTCCTTCCCATGCCCCAACTAATTTTGAGATTC
AGTCAGAAAATATAAATGCTGTATTATA

FIGURE 149

MKILVAFVLVLTIFGIQSHGYEVFNIIISPSNNGGVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSRRACFILKMDHQNI PPLNNLQWYIYEKQALDNMFSNKYTWWKYNP
LESLIKDVDWFLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

FIGURE 150

GGCAGAGCCAGGAAGTCTAGGAGGTTCTCACTGCCCCAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCTGGAAGTTTTCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACGCCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
CAACCTCAACGTCACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCTT
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGCAGGCCCCAGGGTGGA
GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCCTGCCG
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
CCTCACAGTGGTGCCCCAGGTGGTGACAGAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
GCCCCATCCTTGCCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG
GGGTTCAGGATAGGAATGGGGAGGTGAGAGGACGCAAGCAGCAGCCATG**TAGA**ATGAACC
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCTGATTGGGA
GTTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPITNSLIGKDGQVHLQQRPCRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVPVPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCTTAATGGCAGCAGCCGCCCTACCAAGATCCTTCTGTGCCTCCCCTTCTGCTCCTG
 CTGTCCGGCTGGTCCC GGCTGGGCGAGCCGACCCCTACTCTCTTTGCTATGACATCACCGT
 CATCCCTAAGTTT CAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
 CTTTTTCTTACTATGACTGTGGCAACAAGACAGTCACACCTGT CAGTCCCCTGGGGGAAGAAA
 CTAATGTGCACAACGGCCTGGAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT
 TACAGAGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCCCTGC
 AGGCAAGGATGTCTTGTGAGCAGAAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
 TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
 CTGGAGCCAAGTGCAGGAGCACCACTCGCCATGTCTCAGGCACAACCCAACTCAGGGCCAC
 AGCCACCACCTCATCCTTTGTGTCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCCTGGCA
 TCTGAGGAGAGTCCCTTTAGAGTGACAGGTTAAAGCTGATACAAAAGGCTCCTGTGAGCAGC
 GTCTTGATCAAACCTCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGATATGTCAGT
 GGCCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCAGTCGCTTGATTTCCTT
 TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
 TGATGGAATTCCTGCACCTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTCT
 TCTTTTGTGTTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAAATGATATT
 GTCAGTAAAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTCCGTGTCTGAAAGAG
 AATTTTAAATTTAATAAGAAAAAATTTATATTAAATGATTGTTTCTTTAGTAATTTAT
 TGTCTGTACTGATATTTAAATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTF
HYDCGNKTVTPVSPLGKKLVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTTCGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCCTCACAAATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAAATGGGAG
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTG
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTTGGGAGGCCAAC
CCACAGAACAGCATTTCTGGGCCAGGCTGTAATCAGAATTGTGCTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCTGTAT
CATCCTTTTCAATAAACTGTATTTCATTTTGAAAAA

FIGURE 155

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FIGURE 156

GTTCTCCTTTCCGAGCCAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATG**GAAG
 CTCTTGTGGCAGGTAACGTGTGCACCACCACACCTGGAAATGCCATCCTGCTCCCGTTCCGTCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGCCCC
 AGAACTGCCCTCCGTTTGTCTCGTGCAAGTAAACAGTTTCAAGCAAGGTGGTGTGCACGCGCCGG
 GGCTCTCCGAGGTCGCCGAGGGTATTCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCGGACACCTTCCGCCACCTCCACCACCTGGAGGTCCTGCAGT
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCTTCAACGGCCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTTCGACAACCTGGCTGACAGTCATCCCTAGCGGGGCCCTTTGAATACCTGTCT
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCTCTTACGCCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGAGGGGCTGTCAACCTCAAGTATCTGAACCTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTCAAGGAAACCACT
 TCCCTGAGATCAGGCCTGGCTCCTCCATGGCTGAGCTCCCTCAAGAAGCTCTGGGTCTATG
 AACTCACAGGTCAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAACT
 CAACTTGGCCCAACAATAACCTCTCTTCTTTGGCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTTGCATCTACACCACAACCCCTTGGAACTGTGATTGTGACATCTGTGGGTACGCC
 TGGTGGCTTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCGCTGTCTGCTCCCAT
 GCACATCGGAGGCGCTACCTCGTGGAGGTGGACCAGGCGCTCCTTCCAGTGCTCTGCCCCCT
 TCATCATGGAGCGACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACTTAAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTGTGCTGCCAATGGGACAGTGCTCAGCCACGCG
 CTCGCCCAACCCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTTCCACGCTGCTGC
 TTTCAAGACTGGGGTGACACATGCATGGTGACCAATGTTGACAGGCAACTCCAACGCCCTCG
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTCAACCAAGT
 AACAGTGGAGACCGGAGATCTCGCCTGAGGACACACGCGGAAAGTACAAGCCTGTTCCTA
 CCACGTCCACTGGTTACCAGCCGGCATATACCACCTTACCACGGTGCTATTACAGACTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCCTGACAAGATGCAGACCAGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACCAAGCAGCGGAGTACAGTC
 ACAGCCGCGCCGACTGTTGAGATAATCCAGGTGGACGAAGACATCCCGACGAGCAACATCCGCG
 AGCAGCAACAGCAGCTCCGTCGGTGTATCAGGTGAGGGGGCAGTGTGCTGCCACAATTC
 ATGACCATATTAACACCAACCTACAAAACGACACATGGGGGCCACTGGACAGAAAACAGC
 CTGGGGGAACCTCTGCAACCCACAGTCACCACTATCTCTGAACCTTATATAATTTCAGACCCA
 TACCAAGGACAAGGTACAGAGAACTCAAAAT**TGA**CTCCCTCCCCCAAAAACCTTATAAAAT
 GCAATAGAATGCACAAGAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTTCTTGTA
 TATGCTTATATATTAAGCTATGGGCTGGTTAAAAAAACAGATTATATTAATAATTTAAAGA
 CAAAAGTCAAAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAATAAAASAGPQNCPSVCSCSNQFSKVVC
 TRRGLSEVPQGI PSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
 LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
 ISEGA FEGLFN LKYLNLGMCNIKDMPNLTPLVGLEELEMSGNHFP EIRPGSFHGLSSLKKLW
 VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLP HDLFTPLRYLVELHLHHNPWNCD CDILW
 LAWWLREYIPTNSTCCGRCHAPMHRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
 KCRTPPMSSSVKWL LPNGTVLSHASRHPRISVLNDGT LNF SHVLLSDTGVYTCMVTNVAGNSN
 ASAYLNVSTAE LNTSNYSFFT TVTETEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
 TTRVPKQVAVPATDTTDKMQTSLDEV MKTKIIIGCFVAVTLAAAMLIVFYKLRKRHQQRS
 TVTAARTVEIIQVDEDI PAATSAATAAPSGVSGEGAVVLP TIHDHINYNTYKPAHGAHWTE
 NSLGNLSLHPTVTTISEPYIIQTHTKDKVQETQI

FIGURE 158

FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNNSYVLSGNEKRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLH
QLYSAAFSKQKLQSAPTKKPALPFGDLPBGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAHCVTDLGKVTMIKTADLKVVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSFSQESHITVAGWNVLADVRSPGFKNDTLRSG
VVSVDVSLLC EEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMGLVSWSYDKTCSHRLSTAFTKVL PFKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAAGCTCAACTTGA
 AGCTTTTCTTGCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGC
 TTCAACCTGACTTTCCACCTTTCTACAAATTCCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTTGGGTGGGCCACCACTAAGTACTTTCGTGGGTGCCATTCAAGAGATTCTCTAAAG
 CAAAGGAGTTTCATGGCTAATTTCATAAGACCCCTCATTTTGGGGAAGGAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACTGCTCTTCTGTGTCTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACCTTGGGAAGAGGTACAGGCAGAAAAATC
 CCAAAGTGTCCAGAGGCCGGTATGCCCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGT
 TTAATCGAGCCAACTCTTGAATGTGGCTATCTAGAAGCCCTCAAGGAAGAAAAATTGGGAC
 TGGCTTTATATTCACGATGTGGACCTGGTACCCGAGATGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTCAGAGTGAATGGATTCTCT
 AACAACTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG
 AATGAAAAATTTCCGGCCCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG
 ACAAAGGCAATGAGGTGAACGAGAACGGATGAAGCTCTTACACCAAGTGTACAGAGTCTGG
 AGAACAGATGGGTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCAGAGTGGATTTCTGGTTGGTGCATTGACCCTGGATCTTTGGTGATGTTTGG
 AAGAACTGATTCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTACAGCTCATTTGTTGAGCTGAATTTTTCTTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAACAGCTTGTAAACAGACAGCTTCTTAGTCATTTTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAATAAGACTGCTGAATGCTGTGAGAGAACCAGAGTTGTTCT
 CGTCCAAGGTAGAAGGTACGAAGATACAATACTGTTATTCTATTATCTGTACAATCATCT
 GTGAAGTGGTGGTGTCAAGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAGGCCACGAATCA
 GGACACAGTGAAGTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAG
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAATAATA
 TGTCTATCAAACTCTGTAGTAAATGTGAAAAAGCAAAA

FIGURE 161

MGFNLT FHL SYKFRLLLLLTLC LTVVGWATS NYFVGAIQEIPKAKEFMANFHKTLILGKGKT
 LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
 AILVPHRNRKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEEN
 WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVG RNSTGYRLRYSGYFGGV TALSREQFFKVNG
 FSNNYWG WGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
 VWRIDGLSSCSYKLVSV EHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCGGGGTGCGCGAGCGGGCTGTGGGCGCGCCGGAGGAGCGACCGCGCAGTTCTC
 GAGCTCCAGCTGCATTCCCTCCGCGTCCGCCCCACGCTTCTCCCGCTCCGGGCCCCGCA**ATG**
 GCCCAGGCAGTGTGTGTCGCGCTCGGCCGCATCCTCTGGCTTGCCTGCCTCCTGCCCTGGGC
 CCGGCGAGGGGTGGCCGAGGGCTGTATGAACCTCAATCTCACCACCGATAGCCCTGCCACCA
 CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGCCCAAGGACAACGGCAGCCTGGCCCTG
 CCGCGTGACGCCCCACTTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA
 GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTCGGCCACGTGCCCGGGGAATTCCCGG
 TCTCTGTCTGGGTCACTGCCGTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG
 GTCTCTCCCATCACAGAGTTCTCTGTGGGGGACCTTGTGTACCCAGAACACTTCCTTACC
 CTGGCCAGCTCCTATCTCACTAAGACCGTCCCTGAAAGTCTCCTTCTCCTCCACGACCCGA
 GCAACTTCCTCAAGACCGCCTTGTCTCTACAGCTGGGACTTCGGGGACGGGACCCAGATG
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTCACCGTGAAGCT
 CAAAGTGGTGGCGAGTGGGAAGAGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
 CCGGGGACTTCTCCGCCTCGCTGAAGCTGCAGGAAACCCCTTCGAGGCATCCAAGTGTGGGG
 CCCACCCATAATTACAGACTTCCAAAAGATGACCGTGACCTTGAACCTTCCTGGGGAGCCCTCC
 TCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCTCCTCCGCTGGAGGAAGGGGAGTGCCACC
 CTGTGTCGTGGCCAGCAGCGTACAACCTGACCCACCTTCAGGAGCCCTGGGACTAC
 TGCTTCAGCATCCGGGCGGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGT
 GTGGCCCTCCAGAATCCAGCCGGCTGTCTTGGCTTTCCTATGTGCTACACTTATCACTGTGA
 TGTGTGGCTTTCATCATGTACATGACCTGCGGAATGCCACTCAGCAAAAAGGACATGGTGGAG
 AACCCGGAGCCACCCCTCTGGGGTCAAGTGCTGCTGCCAGATGTGCTGTGGGCCCTTCTGTGT
 GGAGACTCCATCTGAGTACCTGGAATTTGTTCTGTGAGAACCACGGGCTGCTCCGCCCCCTCT
 ATAAGTCTGTCAAACTTACACCGTG**TGA**GCACTCCCCCTCCCCACCCCATCTCAGTGTAA
 CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGACCACTGACCAGGAGGGGTTCATT
 TGGCTGGGGCTGTTGGCCTGGATCATCATCTCATCTGTACAGTTGACCCACTGCCACAAGCC
 CCTCCCTCTGTGTCACCCCTGACCCAGCCATTACCCATCTGTACAGTCCAGCCACTGACA
 TAAGCCCACTCGGTTACACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGTCAGGACT
 TTGATGCTTGGGGTGTCCGTGTTGACTCCTAGGTGGGCTGGCTGCCCACTGCCCATTCCT
 CTCATATTGGCACATCTGCTGTCCATTGGGGGTCTCAGTTTCTCCCCAGACAGCCCTAC
 CTGTGCCAGAGAGCTAGAAAGAAGGTCATAAAGGGTTAAAAATCCATAACTAAAGGTTGTAC
 ACATAGATGGGCACACTCACAGAGAGAAGTGTGCATGTACACACACCCACACACACACACA
 CACACACACACAGAAATATAACACATGCGTCACATGGGCATTTTCAGATGATCAGCTCTGTA
 TCTGGTTAAGTGGCTTGTCTGGGATGCACCTGCCTAGAGCTGAAGGAAATTTGACCTCCA
 AGCAGCCCTGACAGGTTCTGGGCGCGGCCCTCCCTTTGTGCTTTGTCTCTGCAGTTCTTGC
 GCCCTTTATAAGGCCATCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACT
 AATCTAGTGATTTGCAGAGTGCTTTATAAATACACCTTATTTTTCGAAACCCATCTGTG
 AAACCTTTCACGTAGGAAAGGCTTGCAGCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGCGG
 TGGCTCACGCCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACGAGATCAGGA
 GATCGAGACCACTCGGCTAACACGGTGAACCCCGTCTCTACTAAAAAATAACAAAAGTT
 AGCCGGGCGTGGTGGTGGTGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAGGAGAATG
 GTGCAACCCGGGAGGCGAGCTTGCACTGAGCCAGATGGCGCCACTGCACTCCAGCCTGA
 GTGACAGAGCGAGACTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWPAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLWPSSYLTKTVLKVSFLLHDPNFKLTALFLYSWDFDGTQ
MVTEDSVVYYNYSIIIGTFTVKLKVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFAFPATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCCMCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 165

MALSSQIWAACLLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
EPICIFCCGCCCHRSKCGMCKKT

FIGURE 166

CTGT CAGGAAGGACCCTCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCCTGGC
 CTGGATCTTCCACC**ATG**TTCCCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCCTCTTCAACCCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTTGG
 AGTCTCCCTTTGGTATCCGCAAACTCTACATGAAAAGTCTGTTAAAAATCTTTGGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAAGCTTTACAAGCCCTACACCAAC
 GGAATCATTGCAAAGGATCCCACCTTCACTAGAAGAAGAGATCAAAGAGATTTCGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTTCGAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAGGAATGGAGACCATTATGGATGATGAGGTGACAAGAGATTCTCAGCAGAAGAACTG
 GAGTCCTGGAACCTGCTGAGCAGAACAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCCCTGTGGGGTTAGGAGTGTGATTCCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTCACAGGGATTAGCCTTCTGGTGGTGGGCACAACTGTGGTGGGATACTTGCCAAAT
 GGGAGGTTTAAGGAATTCATGAGTAACATGTTCACTTAATGTGTTACCGGATCTGCGTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAAACAGACCAAGAATGGTGGCATCT
 GTGTGGCCAATCATACCTCACCAGTCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGCACGGGGGACTCATGGGTGTGATTGAGAGAGCCATGGGTGAAGGCCCTG
 CCCACAGCTCTGGTTTGAAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCATCCTCATCTCCCAAGGAACCTGCATC
 AATAATACATCGGGTATGATGTTCAAAAAGGGAAGTTTTGAAATTGGAGCCACAGTTTACCC
 TGTGTGCTATCAAGTATGACCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAATACGGGA
 TGGTGACGTACCTGCTGCCAATGATGACCAGCTGGGCCATTGTCTGACGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTTCGCAATAGGGTGAATCTGC
 CATTTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAAACCAC
 AAGGACAGGAGCCGCTCCT**TGA**GCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA
 CGGGCTCAGAGCTGAGTTGCGCGCGCCGCCCTGCTGTGTCCTTTCCAGACTCCAGGG
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTTCGCCGAGCCGACAGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCCCTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCTTGTTCCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAAC'TCCCCA
 CCTTTGACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTGTGCTAGAGAT
 GGCCTGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCG
 CTCTCCAGGAAGGCACAGCTGAGGCACTGTGGCTGGCTTCGGCCCTCAACATCGCCCCCAGC
 CTTGGAGCTCTGCAGACATGATAGGAAGGAAACTGTCATCTGCAGGGGCTTTCAGCAAAATG
 AAGGGTTAGATTTTTTATGCTGCTGCTGATGGGGTTACTAAAGGGGGGAAGGAGGCCAGGTG
 GGCCTGTGACTGGGCCATGGGAGAACGTGTGTTCTGCTACTCCAGGCTAACCCCTGAAC'TCCCC
 ATGTGATGCGCGCTTTGTTGAATGTGTGTCTCGGTTTCCCCATCTGTAATATGAGTCGGGGG
 GAATGGTGGTGATTCTTACCTCACAGGCTGTTGTGGGGATTAAGTGTGCTGCGGGTGAGTGA
 AGGACACATCACGTTTCAGTGTTTCAAGTACAGGCCCAAAACGGGGCAGGGCAGGCCCTGAG
 CTCAGAGCTGCTGCACTGGGCTTTGGATTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA
 TGA

FIGURE 167

MFLLLPFDLIVNLLGISLTVLFTLLLVFTIIVPAIFGVSEFGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLIEEEIKEIRRGSSSKALDNTPEFELSDFYFCRKGME
TIMDDEVTKRFSAEELSWNLLSRTNYNFYISLRLTVLWGLGVLRICYFLPLRLALAF TG
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAITYHDRENRPNGGICVANH
TSPIDVILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMV TYL
LRMMTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF
KEEQQKLYSKMIVGNHKDRSRS

FIGURE 168

GCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCA
CGTCTCCTCCAGGATGGCCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC
ACCTGGCAGGCCAGGCTGTTCACCACATCTGCCCTGGGCCTGGCTCCAGACACCTTTGA
CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
AAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCCAGGAGACCTGGGAGGAC
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT
CTACACCAACTCATCGAACACCTTGTAAGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
GCTCCCGGGAGCTCTACATGAGGCACTTCCCTTCAAGGCCCTGCATTCTACCTGATCCGG
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCGG
AGGTGTGGGCAGCCTTCGCTTTGAACCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGGCGGGGCTGT
GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCTCCTCTCTGCCCCCCTG
GAAGACTCTGCTCTTGGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTTGGGCCCCTGAAGTCCA
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCCAACCCAGG
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTCTGCTATGTGATGGGGACTTCCT
GGGACAAGCAAGGAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
TGGAGTTTTATTGAGGTAGCTACGTGATTAATGGTATTGCAGTGTGA

MALAALMIALGSLGLHTWQAQVPTILPLGLAPDTFDDTYVYGCAEEMEKEAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLPFGFKAQNGIAIMVYTNSSNTLYWELNQAVRTGGGSRRL
YMRHFFPKALHFYLIRALQLLRGSGGCSRGPGEVVFVRGVSLRFEPKRLGDSVRLGQFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKTLTLLAPGEFQLSGVGP

FIGURE 170

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGGCTGGTTCCTCCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAAGAGCTG
GTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
TATTGTCTGGACCTTCAACACAACCCCTCTTGTACCATACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCTCCCCATCTCCTGGAGATGGGGAGAAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCCCTCCATGGTCCCTCTGTGTCTCCTGTTGGTGCCCT
CCTGCTCAGTCTCTTTGTACTGGGGCTATTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAACTCCTAACATATGCCCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACATAATAGAACAATCCTAAAGGAAGA
TCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGATGGAAAAATCCCCACTCAC
TGCTCACGATGCCAGACACCAAGGCTATTGCCTATGAGAATGTTATCTAGACAGCAGTG
CACTCCCCTAAGTCTCTGCTCA

FIGURE 171

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIIVTQNRNRERVDFFDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENV I

FIGURE 172

CTGGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
 TCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
 CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTGTCAACATAC
 AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGTAGACTTCCCA
 GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
 GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
 AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
 ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
 GGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG
 AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCGTGCAGCAGAACTTCTCAAGCCCC
 ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCCTCCT
 GTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTCTTTGTTTC
 TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAA
 ACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
 TAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAA
 AGATGGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTGTCCTATGAG
 AATGTTATCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
 GCTGTGTTTGGGACTGACCCTAGTCTGTGCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
 ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
 GAAAAGATAGAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGAGAGAA
 TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
 CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTACT
 ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAAACGAAAAGGATGGGGA
 AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
 GGTTTGCACAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
 GCCAATCGCTGCCTCCAGGCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC
 ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTATAAATTC
 TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCAGTCTATCAACATGTTACC
 TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCTTGACAAT
 TTTTCATGAAATTATTCCTCTTCCTGTTCAATAAATGATTACCCCTTGCACCTTAA

FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
 TGGATTACGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
 TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
 CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
 AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTCAGTGTGATCA
 CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCCTCTC
 ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
 CATTATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
 GTTTCATAAACCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
 TTCGATTCTGAAGAAAACAACATAGGCTTATCCACTTCTCAGTATTTTtaggtctattgct
 TGTGTGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTGGCTGTC
 TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA
 TCAGTAGTTTGAAAAAAAAA

FIGURE 176

MTCCGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNSPSNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDEENKHRL
IHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

FIGURE 177

GTCCAATCCAAATCACTCATTTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAAGCCAAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGAAAATAGTGAA
AAAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTCAACGACACC
CTGATCTTCACTAAAAATGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNQLQVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTC
GAACTGTGACCATGGAGAGAGTGACCCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCCAGCACCTCCTCCCCGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAAACTCG
CCCCACCACCCCTCA

FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCC
 TGGCTGGGCCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
 CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAAGTGGCCGGGCTCC
 AGTGTTCACAGCCCCCAAACGGAACTGGTTTGGGGTCACCTGGGCCTGATCACTCCT
 ACAGAGGAGGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCACAGGGGCTTTACGGT
 ATGGCTGGGTCCCATCATCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAAGTGGAGCGCCACCGTCGGATGCTGAC
 GCCCGCCTTCCATTCAACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
 TCAGGAGAGGCCCAGTGAATATATTGCCACCATCTTGAGGCTCAGTGCCCTTGTAGAGAAAA
 GAAGCCAGCATATCTCCAGCAGATGGACTTCTGTATTACCTCTCCCATGACGGGCGGCGC
 TTCACAGGGCCTGCCGCTGGTGCATGACTTCACAGACGCTGTATCCGGGAGCGCGCTCG
 CACCCTCCCCACTCAGGGTATTGATGATTTTTCAAAGACAAGCCAAGTCCAAGACTTTGG
 ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
 CTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCC
 TTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
 ATGCTGCAACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAGGCATTACCTGCC
 TCATCGATATTATAGGGGTCCATCACAACCCAAGTGTGGCCGGATCTGAGGTCTACGAC
 CCCTTCGGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCCTTTCTC
 CGCAGGCGCCAGGAACTGCATCGGCGAGCGTTGCGCATGGCGGAGATGAAAGTGGTCTCGG
 CGTTGATGCTGCTGCACTTCCGGTTCCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAA
 TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCGAATGTAGGCTTGCA
TGACTTCTGACCATCCACCTGTTTTTTTGAGATTGTCATGAATAAACGGTGTGTCAAA

MSLLSLPWLGLRPVAMSPWLLLLLVGSGWLLARILAWTYAFYNNCRRLQCFQPQPPKRNWFVG
HLGLITPTEEGLKDSQMSATYSQGFTVWVLGPIIPFIVLCHPDTIRSI TNASAAIAPKDNLF
IRFLKPWLGEIGILLSGGDKWSRHRMLTPAFHFNLKSYITIFNKSANIMLDKWQHLSSEGS
SRLDMEFHTSLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFRHRACRLVHDFTDVAVIRERRRTLTPQGIDDFKDKAKSKTLDIFDVL LLSKDEDG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCRQEVQELLKDRDPKEIEW
DDLAQLPFLFTMCVKESLRHLPAPFISRCTQDIVLPDGRVIPKGITCLIDIGVHHNPTVW
PDPEYVDPRFDENSKRSPLAFIPISGAPRNCIGQAFAMAEMKVVLMLMLLHFRFLPDHT
EPRRKLELMRAEGLGLWRVLEPVLNGLO

FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGCTCTATCTTGTGGCGATC**CATG**TATAAGCTGGCCTCCTGC
 TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCCTCTCCTTGACTCCAGGGA
 AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGGAGGAGCTAGAAA
 GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAAGAGGGGATATTCTCAGG
 AAAGCAGACTCAAGTACCAACATTTTAAACCAAGAGGAAAATTTGAGAAAGTTTCAGGATTT
 CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAACCATACA
 AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGT**CTGA**AGTGAAATAAGCATCTGT
 TAGTCAGCTCAGAAACCCCATCTTAGAATATGAAAAATAACACAATGCTTGATTTGAAAC
 AGTGTGGAGAAAACTAGGCAAACTACACCCTGTTTATTGTTACCTGGAAAATAATCCTCT
 ATGTTTGCACAAAAAAAAAAAAAA

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FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

200-
500-
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300-
350-
400-
450-
500-
550-
600-
650-
700-
750-
800-
850-
900-
950-
1000-

FIGURE 185

GAACATTTT TAGTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAATGCAGGCCCCACCTGTCTGCAACCCAGCTGAGGCC**ATG**CCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGCCCATGGCAGGCT
CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAG**TGAT**CGCCCCACAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAACGTGA

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FIGURE 186

MPSPGTVCSELLLGLWLDLAMAGSSFLSFEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDLEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

$\frac{p_{n+1}}{q_{n+1}}$
 $\frac{p_{n+1}^{(1)}}{q_{n+1}^{(1)}}$
 $\frac{p_{n+1}^{(2)}}{q_{n+1}^{(2)}}$
 $\frac{p_{n+1}^{(3)}}{q_{n+1}^{(3)}}$
 $\frac{p_{n+1}^{(4)}}{q_{n+1}^{(4)}}$
 $\frac{p_{n+1}^{(5)}}{q_{n+1}^{(5)}}$
 $\frac{p_{n+1}^{(6)}}{q_{n+1}^{(6)}}$
 $\frac{p_{n+1}^{(7)}}{q_{n+1}^{(7)}}$
 $\frac{p_{n+1}^{(8)}}{q_{n+1}^{(8)}}$
 $\frac{p_{n+1}^{(9)}}{q_{n+1}^{(9)}}$
 $\frac{p_{n+1}^{(10)}}{q_{n+1}^{(10)}}$
 $\frac{p_{n+1}^{(11)}}{q_{n+1}^{(11)}}$
 $\frac{p_{n+1}^{(12)}}{q_{n+1}^{(12)}}$
 $\frac{p_{n+1}^{(13)}}{q_{n+1}^{(13)}}$
 $\frac{p_{n+1}^{(14)}}{q_{n+1}^{(14)}}$
 $\frac{p_{n+1}^{(15)}}{q_{n+1}^{(15)}}$
 $\frac{p_{n+1}^{(16)}}{q_{n+1}^{(16)}}$
 $\frac{p_{n+1}^{(17)}}{q_{n+1}^{(17)}}$
 $\frac{p_{n+1}^{(18)}}{q_{n+1}^{(18)}}$
 $\frac{p_{n+1}^{(19)}}{q_{n+1}^{(19)}}$
 $\frac{p_{n+1}^{(20)}}{q_{n+1}^{(20)}}$
 $\frac{p_{n+1}^{(21)}}{q_{n+1}^{(21)}}$
 $\frac{p_{n+1}^{(22)}}{q_{n+1}^{(22)}}$
 $\frac{p_{n+1}^{(23)}}{q_{n+1}^{(23)}}$
 $\frac{p_{n+1}^{(24)}}{q_{n+1}^{(24)}}$
 $\frac{p_{n+1}^{(25)}}{q_{n+1}^{(25)}}$
 $\frac{p_{n+1}^{(26)}}{q_{n+1}^{(26)}}$
 $\frac{p_{n+1}^{(27)}}{q_{n+1}^{(27)}}$
 $\frac{p_{n+1}^{(28)}}{q_{n+1}^{(28)}}$
 $\frac{p_{n+1}^{(29)}}{q_{n+1}^{(29)}}$
 $\frac{p_{n+1}^{(30)}}{q_{n+1}^{(30)}}$
 $\frac{p_{n+1}^{(31)}}{q_{n+1}^{(31)}}$
 $\frac{p_{n+1}^{(32)}}{q_{n+1}^{(32)}}$
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 $\frac{p_{n+1}^{(34)}}{q_{n+1}^{(34)}}$
 $\frac{p_{n+1}^{(35)}}{q_{n+1}^{(35)}}$
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 $\frac{p_{n+1}^{(37)}}{q_{n+1}^{(37)}}$
 $\frac{p_{n+1}^{(38)}}{q_{n+1}^{(38)}}$
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 $\frac{p_{n+1}^{(40)}}{q_{n+1}^{(40)}}$
 $\frac{p_{n+1}^{(41)}}{q_{n+1}^{(41)}}$
 $\frac{p_{n+1}^{(42)}}{q_{n+1}^{(42)}}$
 $\frac{p_{n+1}^{(43)}}{q_{n+1}^{(43)}}$
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 $\frac{p_{n+1}^{(67)}}{q_{n+1}^{(67)}}$
 $\frac{p_{n+1}^{(68)}}{q_{n+1}^{(68)}}$
 $\frac{p_{n+1}^{(69)}}{q_{n+1}^{(69)}}$
 $\frac{p_{n+1}^{(70)}}{q_{n+1}^{(70)}}$
 $\frac{p_{n+1}^{(71)}}{q_{n+1}^{(71)}}$
 $\frac{p_{n+1}^{(72)}}{q_{n+1}^{(72)}}$
 $\frac{p_{n+1}^{(73)}}{q_{n+1}^{(73)}}$
 $\frac{p_{n+1}^{(74)}}{q_{n+1}^{(74)}}$
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 $\frac{p_{n+1}^{(76)}}{q_{n+1}^{(76)}}$
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 $\frac{p_{n+1}^{(95)}}{q_{n+1}^{(95)}}$
 $\frac{p_{n+1}^{(96)}}{q_{n+1}^{(96)}}$
 $\frac{p_{n+1}^{(97)}}{q_{n+1}^{(97)}}$
 $\frac{p_{n+1}^{(98)}}{q_{n+1}^{(98)}}$
 $\frac{p_{n+1}^{(99)}}{q_{n+1}^{(99)}}$
 $\frac{p_{n+1}^{(100)}}{q_{n+1}^{(100)}}$

FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCTCCTCGTCCAGTACCTC
 GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAAATATGAACACGTGGTGTCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG
 CTCCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCCCCACCCCTAAGCCCCCGATCCCCCAAGGTGGGTGGTCAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCCTGAGCCCCCACGCCCTGGGGCCAGAGTCTTT
 GTCCCCCGTGTGCGCATGTGTTCAGGGTCAGCCTCTCCAGAAGTGAGATCATGGACAAAAA
 GGGCAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTCAGA
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAACACAAGTAGAAATTTCTAACATGAAATATATTACAGGCAGGTCACCCACTAACCA
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCAGAGTGGGCACAGCGGTAGGCGGTC
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACACCTCCCTGCTCCTGGCACCAGCCGTTTTTGGTCATGGTGGGCCAGCTGCAAAAGCG
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCTGCTCAGGGCAGAGGAGTTGGGTGGGTCAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCTTGCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGA
 GCCTCCTTGTTTCATAACCACAGGTTACCCCTACAAACCACTGTCCCCACACAACCTTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCCTCCAGACAAGCTGCAAGACGCTGACC**ATG**GCCAAAG
 ATGGAGCTCTCGAAGGCCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATAACAACCTGGGAGACTGGGGATGA
 CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAAACTGTGGAAG
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAAGTTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTCCCTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTATCATCAGCTTCTCTCTGCT
 ACTAACAGACTTGCTACTCACTGGGAACCCCTGCCGTGGGCTCAAACCTGAGCGCTTTTGCTG
 CTGTTTCTCTGTCTGTCTCAGGTCTCTCTGGGGATGGTGGCCACATGATGTATTACAAGTC
 TTCCAAGCGACTGTCAACTGGGTCCAGAAGACTGGAGACCACATGTTTGAATATAGGCTG
 GGCTTTACATGGCTGGCTCTCCTTCACTGCTGCATGGCGTCGGCTGTACCACCTTCA
 ACACGTACACCAGGATGGTGCTGGAGTTCAAGTGCAAGCA**TAG**TAAAGAGCTTCAAGGAAAAC
 CCGAAGTGCCTACACATCACCATCAGTGTTTCCCTCGGGCGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
 AAAGAAGCAGTTAGGTCACTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGA
 GTAGGCTTGAGCCCTACCTTACACGTCGTCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGATTCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTCACCCAC
 CCCACATCTCACATCCAGAATCCCTTCTTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC
 TAAACCATGGAGATAAAAAGAAGAGTAAAATACACTCCCGACCTTAAGGATCTGAAA

FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTNSTQEVVQYNWETGDDRF'SFRSFRSGMWLSCETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTS IHQL
PPATNRLATHWEPCLWAQTERLCCCF LCPVRS PGDGGPHDVFTSLPDCQLGSRRLETTCL
LWLGLLHGLALLHLLHGVGCHHLQHVVHQDGAGVQVQA

FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCAGATG TGGTTACCCCTTGGTCTCCTG
 TCTTTATGTCTTTCTCCTCTTCTATTTCTGTCACTCTCCCTCACTTAAGTCTCAGGCCTGTCA
 GCAGCTCCTGTGGACATTGCCATCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
 TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
 GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
 AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCCTCCCAA
 GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
 CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
 AGCCACCTCCCTGTCAGCCAGTATTAAATGTCCCCTTCCCCCTGCCCGCCGTAGATTCAG
 GACATTGCCCCCTGTGTGCCACCAACCAGGACTTCCCCTTGGCTTGGCATCCCTGGCTCT
 CTCTGGTACCCAGCAAGACGTCTGTTCAGGGCAGGTAGCATCTTCAAGCTCCGTTACT
 ATGGCGATGGCCATGATGTTACAATCCCACTTGCCTGAATAATCAAGTGGGAAGGGGAAGCA
 GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTGAGGAAAAACCAA
 GGGGAAGCAACAGGAACCTTCTGCAACTGGTTTTTATCGGAAAGATCATCTGCTGCAGATGC
 TGTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA
 ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAAACTCTTTATTACTTTGGG
 AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAAACCCAGTGATTACCTGCTGG
 AACCAGGAAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
 CATGCCACCAAAACAATAAAACAAAATTCTTAACACTGAAA

MWLPLGLLSLCLSPILSSPSLKSQLQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGSME
HRNHLCFCDLDRATSPPLKCSLL

1000 900 800 700 600 500 400 300 200 100 0

FIGURE 193

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGTGCTGCCGCCGCCGCTCGGGTCTGGAGCCAGGAGCAGCTCA
 CGCGC**ATGG**CAGGCATCAAGCTTTGATTAGTTTGTCCCTTTGGAGGAGCAATCGGACTGATGTTTGTGATGCTT
 GGATGTGCCCTTCCAATATACAAACAATACTGGCCCTCTTTGTCTATTITTTTACATCCCTTCCACTATTCC
 ATACYGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTGAAGAACTTGCCACTTTTC
 TTACAAAGGGCATTGTGCTGTACGCTTTTGGACTCCCTATTGATTITGGCAGAGCACTGTGATTGAGTGGGGA
 GCTTGTGCACCTTGTCTCACAGGAACACAGTCACTTTTGGCACTATACTAGGCTTTTCTTGGTCTTTGGAAG
 CAATGACGACTTCAGCTGGCAGCAGTGG**GGA**AAAGAAATTAAGTAATTTGTCAAAATGGAACTTCCCTGTCATTT
 GTTGGCCATTACGCACACAGGAGATGGGCGAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGGTATTTTA
 GGTGCTCCCTTCTCACTTTTATTGTAAAGCATACTATTTTACAGAGACTTGTGTGAAGGATTAAGAGGATTTTCT
 CTTTGGAAAGCTTGACTGATTTTACACTTATCTATAGTATGCTTTTGTGGTGTCTGCTGAATTTAAATAT
 TTATGTGTTTTCTGTAGGTTGATTTTTTGAATCAATATGCAATGTTAAACACTTTTTTAATGTAAATCA
 TTTGCATTGGTTAGGAATTGCAATTCGGCGGCTCTATTACTGGTCAAGTACATCTTTTCTCTTAAATATT
 TAGCCCTCATTATTACAAAAATATAAAAAATAAGTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACGTTATAGACTGTATACTCAGTGCAATATAGCTGCATTATACCTCAGAG
 GGGCCAAAGTGTAATGCCCATGCCCTCCGTTAAGGGTGTGTTGGTTTACTGGTAGACAGATGTTTTGTGGATTG
 AAAATTAATTTATGGAATTGCTACAGAGGAGTGCTTTTCTTCAATTGTTAGAAGAAATTTATGTTAAACTTTA
 AGGTAAAGGTGTAAAAACATTTTGAGATAAGGTTTTTATTATGTTTATTATGTTAGAGTGAGTGGCAATGT
 GGGGAAGAAATGACATTGAAATTCAGTTTTTGAATCCTGTTTCTATTTATAAGTGAATTTGTGATCTCCTATC
 AACCTTTTCATGTTTTACCTGTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGTATGTTTGC
 ATCATATATGCCAGAAACCTTCTCTGCTTCTCCTTTTGACTTATTGGTATGTTGTATATATTACATRAAAA
 TAACCTTTCAATATAGTTTTAATAACACTTGAAGTGTTTACTTACCTGAAAAATTAATGCTATGCCGTACATT
 CAGAGTGCCCTTCCCTGCAAGGCCCTTGCCATGATTAAACAAGTAACTTTAGTCTTACAGATAATTCATGCA
 TTAACAGTTTTAAGATTAGACCATGGTAATAGTAGTTCTTATTCTCTAAGGTTATATCATATGTAATTTAAAG
 TATTTTTTAAGACAAGTTTCCGTGATACCTCTGAAGCTGTTTGTATTTTGAGTCTCATCATGATAGATCTGCTGTT
 CCTTATAAAGGCATTTGTTGTGTAGTTAATGCAAGTAGCCAAAGTCCAGCTATATAGCAGCTCAGAAACAT
 ACCTGACCAAAAAATTCACGATAACAGGCATGATCAATTTATAGTGGTCTTTTACATCTAATAAATATCAGGA
 CTTTTTTCAGAGTGGGTTATAAAAAACATTCAAGTGGTCTCACAGTATTTTGTGAAGGATATTCTCTTCATG
 TTTATTGAGTATACTTTACATAAAAAATTAATTCGCCATCACCCAAAACCTCAGTAATCATGACAGCTGTCTCTGT
 TTTATGAAGTTTATTCTCAAGAAATGCGAATAAATTTGGGATTTGTTCACTTTTACTAAAGATGCCTAA
 AGCCACAGGTTTTATTGCCTAACCTTAAGCCATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAATATCG
 GCGTGTGGCTGGAGCCTTCCCATCGGAGCTGAAGATGGCTTGTGCTATTATAAAGTTTCAGATTTCAGAGGAA
 GGTGCAGGTACACATGAGTTAGAGAGCTGGTGACAGCTTGGGAACCTTTTGTGCTGATCTACTGGACTTT
 TTTTTTGCAGGAAGTGCATTTCTCTGCTTCCCTATTTTCTGTCTGAGTGTGCTGAGTGCAGTGCATCTGACTGT
 TTTTATCCACTTGGCCACAGACTTTTCTAACAGCTGCGTATTATTCTATATCAATTAATGATTTGGCAGCATT
 GTGCTTTGACCTTGTATACCTAGCTTGACATAGTGTCTCTGATTTCTAGGCTTACTTGTAGATATGAAT
 TTTCATAGAAATATGACTGTATACACATATACACTTCTCTATGGAAAGAAACCTTTGTATGATGAACAATAA
 AGATTTTAAGATATCTTTTAAAAAATAA

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FIGURE 194

MAGIKALISLSFPGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

FIGURE 195

FIGURE 196

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAQQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNTTFRMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTELHLEHNDLVKVNFAHFPRLLSLHSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSIT
LAGNLWDCGRNVICALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVYAFHLCEDGAEPTSG
HLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH
IEGALVIINEYGSCTCHQQPARECEV

FIGURE 197

GTGCAAGGAGCCGAGGCGAG**ATG**GGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACCAGGACCCCGTGCGCCGGCGCGCCGTTGAGTTCCCGGCGGACAAGATGG
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGA
CTCGTCCTGGCTTCAGGAGCCGGATTTCGGCGTCTCAGACGTGGGCTCGCACCTGGAATGTGG
CGCGGGCGAACCTGCCGTCTTCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCTGCCCTGCCGC
CACGACGACGTCTTCTTTCGCCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGACGATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTCGGCGTCCGCGCGGGCCGCTACGCTTCCACGGGCCGGGCGCG**CTGA**GCGTG
GGCCCCGAGGACTGCGCGGACCCGTGCGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCT

[illegible][illegible]

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The concentration of the *Agrobacterium* suspension was 10⁶ cells/ml (a), 10⁷ cells/ml (b), 10⁸ cells/ml (c), 10⁹ cells/ml (d), 10¹⁰ cells/ml (e), and 10¹¹ cells/ml (f). The concentration of the *Agrobacterium* suspension was 10⁶ cells/ml (a), 10⁷ cells/ml (b), 10⁸ cells/ml (c), 10⁹ cells/ml (d), 10¹⁰ cells/ml (e), and 10¹¹ cells/ml (f). The concentration of the *Agrobacterium* suspension was 10⁶ cells/ml (a), 10⁷ cells/ml (b), 10⁸ cells/ml (c), 10⁹ cells/ml (d), 10¹⁰ cells/ml (e), and 10¹¹ cells/ml (f).

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The concentration of the *Agrobacterium* suspension was 10⁶ cells/ml (a), 10⁷ cells/ml (b), 10⁸ cells/ml (c), 10⁹ cells/ml (d), 10¹⁰ cells/ml (e), and 10¹¹ cells/ml (f). The concentration of the *Agrobacterium* suspension was 10⁶ cells/ml (a), 10⁷ cells/ml (b), 10⁸ cells/ml (c), 10⁹ cells/ml (d), 10¹⁰ cells/ml (e), and 10¹¹ cells/ml (f). The concentration of the *Agrobacterium* suspension was 10⁶ cells/ml (a), 10⁷ cells/ml (b), 10⁸ cells/ml (c), 10⁹ cells/ml (d), 10¹⁰ cells/ml (e), and 10¹¹ cells/ml (f).

FIGURE 201

TTGAGCGCAGGTGAGTCTCTCGCGTTCGGGGCGTTCCTCCAGTCACCCCTCCCGCGTTACCCGCGGCGCGC
 CCGAGGGAGTCTCTCCAGACCCCTCCCTCCCGTTGCTCCAACTAATACGGACTGAACGGATCGCTGCGGAGGGT
 GGGAGAGAAATAGGGGGAGAAAGGACAGAGAGCACTACCCTCCATAGCCAGATAGATTACTTTACACTG
 AACTGATCAAGTACTTTGAAATAGTACTTCGAATTTATCTTGGTCTCCTCATACTTGTCTGACTGAGTCTTTC
 AACCACTTTTCTCTCCACTAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGATGGATTCCGTTGGGATTA
 TATATAAGTTCCCAACGCCCTTTTCAATATATATGAAATGGTTTACAGTGAAGCAAGTTCAATGTTT
 TTTATTACAAAACCTACCTTAACCATTATACTTTGGTAAGTGGCCTCTTGACAGAGAAATCATGGGATTTGTTC
 AAATGATATGTTTGATCTTATTCGGAACAAATCTTCTCCTTGGATCACATGAATATTTATGATTTCCAAGTTT
 GGGAAAGAGCGACACCAATATGGATCACAAACAGAGGGGAGGACATACATAGTGGTGCAGCCATTTGGCCCCGA
 ACAGATCTAAAAATACATAAGCGCTTCTCTACTCATACATGCCTTACAATGAGTCAGTTTCATTTGAAGATAG
 AGTTGCCAAAATTTGTTGAATGGTTTACGTCAAAGAGCCATAAATCTTGGTCTTCTCTATTGGGAAGACCTG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGGCCTGTCATTTGAGATATTGACAAGAAGTTA
 GGTATCTCATACAAATGCTGAAAAAGGCAAGTTGTGGAACACTCTGAACCTAATCATCACAGTGATCATGG
 AATGACGCGTGTCTGAGGAAGGTTAATAGAACTTGACCACTACCTGGATAAAGACCCTATACCTGATTTG
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAAGGTAATTTGATGAAGTCTATGAAGCACTAACTCAGCT
 CATCTTAATCTTACTGTTTACAAAAAGAAGACGTTCCAGAAAGGTGGCATTACAAATACAACAGTCGAATTC
 ACCAATCATAGCAGTGGCTGATGAAGGGTGGCAGCTTTTACAGAAATAGTCAGATGACTTCTGTTAGGCAACC
 ACGGTTACGATAATCGTTAGCAGATATGCTCCAATATTTTAGCCCATGGTCTGCTTACAGAAAGAAATTC
 TCAAAGAAGCCATGAATCCACAGATTTGTACCACTACTATGCCACCTCTCTCAATATCACTGCCATGCCACA
 CAATGGATCATCTTGGATGTCAGGATCTGCTCAATTCAGCAATGCCAAGGGTGGTCCCTTATACACAGAGTA
 CTATACTCTCCCTGGTAGTGTAAACAGCAGAAATGACCAAGAGGGGTATACCCCTATTTCATAGGGGTCT
 TCTCTTGGCAGCATTATAGTGATTGTATTTTGTAAATTTTCAATAGCATTAAATTCACAGTCAAAATCCCTGC
 CTTACAAGATATGCATGCTGAAATAGCTCAACCATTTTACAAGCCTAATGTTACTTTGAAGTGGATTTGCATA
 TTGAAGTGGAGATTCCTAATATATGTCAGTGTAAAGGTTTCAAATCTGGGAACCAAGTTCACAACTCTGC
 AGAAACCATTAAGCAGTTACATATTTAGGTATACACACACACACACACACACACACACACACACAGGACCAA
 ATACTTACACCTGCAAGGAATAAAGATGTGAGAGTAGTCTCCATTGTTCACTGTAGCATAGGGATAGATAAG
 ATCTGCTTTTATTTGGACTTGGCGCAGATAATGTATATATTAGCACTTTGCACTATGTAAGTACCTTATAT
 ATTGCACTTTAAATTTCTCTCGGTGGTACTTTAAATTTGAAATGCATTTATGGACAGTTATGTCTTATAAC
 TTGATTTGAAATGACAACTTTTGACCCCATGTACAGAACTTGTGTACGCATTGTTCAAACCTGAAGCAAAAT
 TCTAATAATCCGGAATAATGAACATAGAAATCTATCTCCATAAATFGAGAGAAGAAGGTGATAGTGTGTA
 AAATTAATGTGATAACCTTTGAACCTTGAATTTGGAGATGTATCCCAACAGCAGAAATGCAACTGTGGCAT
 TTCTTGTCTTATTTCTTTCCAGAGAAGCTGGTTTTTCAATTTATTTTCCCTCAAAGAGAGTCAATTAATGAT
 ATTCTGTTCTAAATATATTTCTCTCATAAAAATATTTGATTTTCCCTGATGAGTCAATTAATGATGATTTCA
 TAATAATGAAGACACCATGAATATACCTTTCTCTATATAGTTGAGCAATGGCTGAATGAAGCAACAGGCA
 CCATCTCAGCAATGTTTTCTCTTGTGTGAATATTTGTCCTTTGAAAATTAATCATATTAAATACATTAA
 AAATCAAATTGATAAAAA

FIGURE 202

MTSKFILVSFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
 QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRKNKSFSLDHMNIIYDSKFWEETPIW
 ITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
 WEDPDDMGHHLGPDSPLMGPVISIDDKKLGyliQMLKKAKLWNTLNLIITSDHGMTQCSEER
 LIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALHAHPNLTVYKKEDVPERWHYKYN
 SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
 LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYPTQSTILLPGSVKPAEYDQEGSYPYF
 IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLIQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTTGTGATCCGCGATTTCGCTCCCACGGGCGGGACCTTTGTAACGCGGGAGGCCAG
 GACAGGCCACCCCTGCGGGGCGGGAGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCCCTTGCCCTGGGTCACACAGCCAAGGAGGCAGAGCCAGAACTACAA
 CCAGATCCAGAGGCAACAGGGGACATGGCCACCTGGGACGAAAAGGCAGTCAACCGCAGGGCC
 AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCGTGGGAGACGA
 CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGG
 AGCAGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCCTGACGTTGCC
 CCTGCCCCCTGGCCCCGCACCCAGGGCCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT
 CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC
 TTGCTGAGCTCATCTTGACCTGAAGATCATCCAGCCCACAGAATAACTATGCTGCCATG
 GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT
 ATTTGTCTTCCGCCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGG
 TGGTCTCATTCATCCTTGACATTTGTCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
 CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTCAGAACGGCAACTCTTAAGGTTAAACAGATGAATGTACAATTGGCCGCCA
 AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCCTGGACTGATGAGTTTGCTGTATC
 AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAAGTCCTGGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
 TCACCTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAGAAGACAAAACC
 AAAATCTATAAAGATATTCTGAAAATATGACAGAATTGTGACAAATAAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$

$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$

FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCCGCCAACAT
GCTCTGTCTGTGCTGTACTGTCGGGTTCATCGGGGAAGCCAGACCGAGTTCACGACTTTG
 AGTCCAAGGGGCTCCCTGCCAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTATCCCTCC
 CAGGAATTTCTCCACCTAGCCGCTGGAAGCAGAAAAATTGTACAAGCTGGAGATTAAGGACCT
 TGAATGGGCAGCTAGACTTTGAAGAAATTTGTCTATTATCTCCAGATCATGAGAAGAGGCTGA
 GGCTGGTGTTTTAAGATTTTGGACAAAAAAGAAATGATGGACGCATTGACGCCGAGGAGATCATG
 CAGTCCCTGGGGAGTGGGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATTTCTCAAGAG
 CATGGATAAAACGCCAGCATGACCATCGACTGGAAACGAGTGGAGAGACTTACCACCTCTCTCC
 ACCCCGTGGAAACATCCCGAGATCATCTCTACTGGGAAGCATTCCACGATCTTTGATGTG
 GGTGAGAATCTAACGCTCCCGGATGAGTTACAGTGGAGGAGAGGCAGACGGGGATGTGGTG
 GAGACACCTGGTGGCAGGAGTGGGGCAGGGGCCGTATCCAGAACCTGCACGGGGCCCTGG
 ACAGGCTCAAGTGTCTCATGCAGGTCATGCTCCCGCAGCAACAACATGGGCATCGTTGGT
 GGCTTCACTCAGATGATCGAGAGGAGGGGCCAGGTCACCTGGCGGGGCAATGGCATCAA
 CGTCTCAAAATTCGCCCAATCAGCCATCAAAATTCATGGCCTATGAGCAGATCAAGCGCC
 TTGTTGGTAGTGACAGGAGCTCTGAGGATTCACGAGAGGGCTTGTGGCAGGGCTCTGGCA
 GGGGCCATCGCCAGAGACGACATCTCCCAATGGAGGTCTCGAAGACCCGGATGGCGCTGCG
 GAACACAGGCCAGTACTAGGAATGCTCGACTGCGCCAGGAGGATCTGGCCAGAGAGGGGG
 TGGCGGCTCTACAAAGCTATGTCTCCCAACATGCTGGGCTATCCCTATGCCGCGATC
 GACCTTCAGCTTACAGGACGCTCAAGAAATGCTGGCTGCAGCAGTATGAGCTGAACAGCGC
 GGACCCCGGGCTGTTTGTGCTCTGGCTGTGGGCACCATGTCCAGTATCTGTGGCCAGCTGG
 CCAGCTACCCCTGGCCCTTAGTCAGGACCCGGATCGAGCGCAAGGCTCTATTGGAGGCGCT
 CGGAGGTGACCATGACGAGCCTCTTCAAAATATCTTGGCGACCAGGGGGCTCTCGGGCT
 GTACAGGGGCTGGCCGCCAATTCATGAAGTTCATCCAGCTGTGAGCATCAGCTACGTGG
 TCTACGAGAACCTGAAGATCACCTGGCGTGCAGTTCGGG**TGA**CGGGGGGAGGGGCCCGCC
 CGAGTGCAGTCCTGATCTTGGGCCGAGCGTGGGGTGTGCAGCCATCTCATTTCTGTGAATG
 TGGCAACACTAAGCTCTCGACCAAGCTGTGAAAAACCTAGACGCACCCGAGGGAGGGT
 GGGGAGAGCTGCGAGCCGAGGCTGTCTGCTGACCCAGCAGACCTCTCTGTTGGTTCC
 AGCCAAGACCACAGGCAATCTTCTAGGCTCAGGCTCAGCAGGCTCGGGCTCACATGTGTAA
 GGACAGCAATTTTCTGCAGTGCCTGCCAATATGAGTGTGAGCTGTGAGGCCGGCTTAGT
 TCTTCCATTTCACTCTGCAGCCAGCTGTGGGCCAGGCCCTGTGCTCTGCTGCCCTGC
 ATCTCCCTGTGCCCTTCTGCTGCCCTGCTGCTGCTGAGGTGAAGGTGGGAGGGCTACAG
 CCCACATCCCACCTCCCTCTGCTCAATCCCATATCCATGATGAAGTGAAGTCAAGTGGCT
 CCCAGGCTGACTTCCCAACTACAGCATTGACGCCAATTCGCTGTGAAGGAGAGGAAAG
 GATCTGGCCTTGTGTCTACCTGGCATGTGACCCCTGCTGATGGCTGGGGCTCTCGGGCATGT
 TGGGAGTGCAGGGGGCTCGGGCTGCCCTGGCTGGCTGCACAGAAGCAAGTGTCTGGGCTCA
 TGGTGCTCTGAGCTGGCTGGACCTGTGACAGTGGGCGCCACCTCAGAACCAATCAGTCT
 TCCCACTGTGGCATGAGGGCAGTGGAGCACCATGTTTGAAGGCGAAGGACAGGCTTTGT
 GTGTTCTGGGGAGGGAAGAAAAAGTGTGGAGGCTCTTAATATGAGCTTGTGGAAAGGG
 TTTTGTCCAGAAGGACAAGCCGACAAATGAGCAGCTTCTGTGCTTCCAGAGGAAGCAGAG
 GAGCAGGAGCTTGGTGAGTGTCTCAGAGATCTGTTCTGACGCCCTGGGGGTCTGCTGTCCAAAC
 CCAGCCGGGCGCAGGGCGAGCCAGCCCCATCCACTTGTGTCTGCTTGGAACTTATTT
 ATTTTGTATTTTATTTGAACAGAGTTATGTCTTAATATATAGATTTGTTTAAATTAATA
 GCTTGTCTATTTTCAAGTTCATTTTATTATATTTATGTTTATGTTGATTTGACTTCCC
 AAGCCCGCCAGTGGGATGGGAGGAGGAGAAGGGGGCTTGGGCGCTGCAGTACATAT
 CTGTCCAGAAATTCCTTTTGGGACTGGAGGCAGAAAGCGGCCAGGACAGCCCTTG
 GCTCCCTTCTCTTGGCAGGTTGGGGAAGGGCTTGGCCCGAGCTTAGGATTCACAGGTTTGA
 CTGGGGGCGTGGAGAGAGGAGGAGAACCTCAATAACCTTGAAGTGGGAATCCAGTTATTTC
 CTGGCTGCGAGGGTTCTTTTATTCACTCTTTTCTGAATGTCAAGGCACTGAGGTGGCTCT
 CACTGTGAATTTGTGTTGGGCGGGGCTGGAGGAGAGGGTGGGGGCTGCTCTCGCTCCCTCC
 CAGCCTTCTGCTGCCCTTGTCTTAACATGCGCGCCCACTGGCGACTCAGGTTGCACTTCC
 ATTTCCACAGAAATGACCTGATGAGGAAATCTCAATAGGATCAAGATCAATGCAAAAAAT
 GTTATATATGAACATATACTGGAGTCGTCAAAAGCAAATTAAGAAAGAAATTTGAGCGTTAG
 AAGTTGTCAATTTAAAGCAGCTTCTAATAAAGTTGTTTCAAGCTCAAAAAA
 AA

FIGURE 206

MLCLCLYVPVIGEATQTEFYFESKGLPAELKSI FKL SVFI PSQEFSTYRQWKQKIVQAGDKD
LDGQLDFEEFVHYLQDHEKKRLRVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILK
SMDKNGTMTIDWNEWDRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDFTVEERQTGMW
WRHLVAGGGAGAVSRTCTAPLDRCLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI
NVLKIAPESAIKFMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQSSIYPMEVLKTRMAL
RKTGQYSGMLDCARRILAREGVAAFYKGYVFNMLGIIPYAGIDLAVYETLKNWLQHYAVNS
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAASIEGAPEVTMSSSLFKHILRTEGAFG
LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCAGCC**AT**
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATATTATTCTGGCTGGAG
CAATTGCACTCATCATTTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTC
GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTTGAACCTGACATCAA
ACTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
AAGAAGGCAAAGATGAGCTGTGCGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTTT
GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
AAACTGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
CGGTGTGAGGCTCCCCGATGGTTCCCCAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA
GGGAGCCAACCTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACCTCTGAGAATGTGACCA
TGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAAGGCGGAG
TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGCTCTTCTTTCTTTGCCATCAGCT
GGGCACCTCTGCCTCTCAGCCCTTACCTGATGCTAAAA**TAA**TGTGCCTTGGCCACAAAAAAG
CATGCAAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG
TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAACAAGAGCA
AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAAA
GACATATTAGAAGTTGGGAAAATAATTTCATGTGAAGTGTGTTAAGAGTGATAAG
TAAATGCACGTGGAGACAAGTGATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCT
GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG
TAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTTCCA
CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
GGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTATGATGCTTCCAAAGGTGCCT
TGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAA
AA

FIGURE 208

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTD
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVD
QGANFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTESEIKRR
SHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK

FIGURE 209

[illegible]

FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLLQEMKTLFLNTEYLMFPFL
LNQCGSLLYLTASTDLTLAVPICNSLAIFTLLIVKGALGEDIGGKRKLDYCECGTQLCGS
RHTCVSSFPEPISPEWVRTRPFPILFPFLQLFCFLVAIRVPFPWTVWRKTEAGVWD

$$H^1(\mathbb{R}^n, \mathbb{R}) \cong \mathbb{R}^n$$

FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTCGAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
 AATCTAATGGAACCTCCTGTCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTC
 CAACGTCAAGTAACGCCACCTGTCAAGTTCCTGTCTGGTGAACAAGACTCTTGGAGGAGTCA
 TCTTTCGAAAGTTTGAGTGTGCAAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCCT
 TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCCTGAGGTCTTGGGGCTGCACTTTGCCCAGACCCCATTCTGCTTCTCTG
 AGGTCCAGAGCACCCCCCTGCGGTGCTGACACCCTCTTCCCTGCTCTGCCCCGTTTAACTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTCTCTCATTATTA
 AAGCACTGGTTCATTCAGTCCAAAAA

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECFSHANTSCISSSASSSLETPVR
LYQNMFCSAENCSEETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE
CPACYESNGTSCRGKPKWCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFEKANVNSLTPTSAPTTSHNVGSKASLYLLALASLLLRGLLP

FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
 GGGCTTGCCCTCACTGGCCACCCCTCCCAACCCCAAGAGCCAGCCCC**ATG**GTCCCGCCGCCG
 GCGCGCTGCTGTGGGTCTTGTGCTGAATCTGGGTCCCCGGCGGGGGGGCCCAAGGCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGGCCCATGACCCGCAG
 CTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCGGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGCCCGCC
 ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA
 GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
 ATACAGCGGGGAGTTCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTACCCCTCACCCACAG
 CCTATGCCATCTCCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCGTGGCACTGCCAC
 TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTCCGGGCGCCT
 TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAGCCTTGACCTATCAACAATGTC
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACCAACAGTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCACTGTTACAGAGATGCAACCAATA
 GACAGAAACAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTTAGTACAGAAAAACAACTGAAAA
 CACAA

FIGURE 214

MVPAAGALLWVLLNLGPRAAGAQGLTQTPTMQRVSLRFGGPMTRSRSRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAAEELLAATVSTGFSSSAINEDGSSEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQPCPNRLREECPLDTSLCDTNCSQSTTSTRTTTTPFPTIHLRSSPSLPPASPCPALA
FWKRVRIGLEDIWNSLSSVFTEMQPIDRNQR

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
 TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCR
 YRTFVPASSPMYHTCVAFAWVSLNAFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
 TVGLQHPAVVSAFRALLLLMLTVHVSYSLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
 RLPHVRCVNVVLLQLGLSLLLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL
 KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 217

GGCCGCGCTGGAATTGTGGGAGTTGTGTCTGCACCTCGGCTGCCGGAGGCCGAAGGTCCTGTA
CTATGGCTCCCCAGAGCCTGCCTTCACTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTG
CTGATGGCCGCTGCTTACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTGCCCTGAC
CAACCCAGAGAAGAGCAGCACCAAGAAACGGAGAGAAAAAGAAACCAAGCCGAGGAGGAGC
TGGATGCCGAAGTCTTGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGG
CAGGCTGTCCCTGCAGGATCCACGTACGGCTGAATCTTCAGACTGGGGAAGAGAGGGCAAA
ACTCCAATATAGGACAAAGTTCGAAATAATTTGAAAGGCAAAAGGCTGGATATCAACACCA
ACACCTACACATCTCAGGATCTCAAGAGTGCACCTGGCAAAATTCAAGGAGGGGGCAGAGATG
GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTTCCGCCCCATTGA
GGAAGTGAAGAAAGACTTTGATGAGCTGAATGTTGTCTATTGAGACTGACATGCAGATCATGG
TACGGCTGTGATCAACAAGTTCAATAGTTCAGCTCCAGTTTGAAGAGAAGATGCTGCGCTC
TTTGATCTGTAAATATTATTCTTCATCAGATGGACAATGCGCAGGACCTGCTTTCTTTGGTGG
TCTTCAAGTGGTGATCAATGGGCTGAAACAGCAGAGCCCTCGTGAAGGAGTATGCTGCGT
TTGTGCTGGGCGCTGCCTTTTCCAGCAACCCCAAGGTCAGGTGAGGGCCATCGAAGGGGGA
GCCCTGCAGAAGCTGCTGGTCATCTTGGCCACGGAGCAGCCGCTCACTGCAAAGAAGAAGGT
CCTGTTTGCACTGTGCTCCCTGCTGCGCCACTTCCCCTATGCCAGCGGCAGTTCTTGAAGC
TCGGGGGGCTGCAGGTCCTGAGGACCCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTG
CGCGTGGTCACACTGCTCTACGACCTGGTCACGGAGAAGATGTCGCCGAGGAGGAGGCTGA
GCTGACCCAGGAGATGTCCCAGAGAAGCTGCAGCAGTATGCCAGGTACACCTCCTGCCAG
GCCTGTGGGAACAGGGCTGGTGCAGATCACGGCCCACTCCTGGCCTGCCGAGCATGAT
GCCCGTGAGAAGGTGCTGCAGACACTGGGCGTCTCCTGACCACCTGCCGGGACCCTACCG
TCAGGACCCCCAGCTCGGCAGGACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCA
GCCTGGAGCTGCAGGATGGTGAGGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAAC
AGCTTGCTGAAGGAGCTGAGATGAGGGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGA
GGCTGAGGGGTGCCAGCTGGGTGGGCTTCTCAGGCAGGAGGACATCTTGGCAGTGCTGGCT
TGGCCATTAAATTGAAACCTGAAGGCCAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
AAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 218

MAPQSLPSSRMAPLGMMLGLLMAACFTFCLSHQNLKEFALTNPKESSSTKETERTKETAEDEL
 DAEVLEVFHPHTEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFSGGLQVVINGLNSTEPLVKEYAAF
 VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLRITLVQEKGTVEVLAVRVVITLLYDLVTEKMFEEEEAEELTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELGVSNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCCGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTTGGGGTTTCGGTTCCTCCCTCCCTCCCTCCGCTCCCGGGGTCTGGGGTGACATTCACCGCCGCTCTGTTGGGTTGCGGTTGCCACCCCA
CGGGACATCCCAGCTGGCGGCCCTCCATTTGGCTGCTCTGGTGACGGCCCCACCCCTC
TTCCACCTTGACACGAGCATGGGGGGCTGCGGTGTTTTTCGGCTGCACTTTTCGTGCGCTTCGGC
CCGGCCTTCGGCGTTTTCTTGATCACTGTGGCTGGGAGCCCGCTTCGGTTTATCATCTCTGG
CGAGGGGACATTTTCTGGCTGGTCTCCCTGCTCTGGCCTCTGTGCTCTGGTTCACTCTGG
TCCATTGTACCCAGCCGCTCAGATGCCCGGCTCCAGTACGGCCTCTGATCTTTTGGTGTCTGG
GCTCTGTCCTTCTACAGGAGGTGTTCCGCTTTGGCTACTACAAGCTGCTTAAGAAGGCAGA
TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATACCCATCTCCATCCGCGACATGGCT
ATGTTTCTGGCTCTCTCTCCGTTATCATGATGGTGTCTTCTCTGTTATCAATATTTTGGCT
GATGCACTTTGGCCAGGTGTGGTTGGGATCAGTGAGACTACCCATTACCTTCTGACTTC
AGCCTTTGACAGCAGCCATTATCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG
CCTGTGAGGAGGACGCGTATCGGCTTTGGGCTTGGTGGTGGGAGTACCTATCGATCATCG
GGACTGACATTTCTGAACCCCTGGTATGAGGCCAGCTGCTGCCCATCTGACGATCACTGT
TTCCATGGGGCTCTGGGCCTTCACACAGCTTGAGGGGTCCCTCCGAAGTATTACGCGCAGCC
TCTTGTGTAAGGACTGACTACCTGGACTGATCGCCTGACAGATCCCAGCTGCCCTGCCATG
CCCATGACTGAGCCGACGCCAGCCCGGGTCCAATTGCCACATTTCTGCTCTCTCTCTGG
GGTCTACCCCACTACCTCCAGGTTTGTCTTGTGCTTTTGTGACGGCTTAGTCTTAAGTCT
TACAGGAGCGAGCTGGGTTCAGCCAGTCACTGATGCTGGTGGTTTGAATCGACTTATCCC
CACCACCTGGGGACCCCTTGTGTGTCAGGACTCCCTCTGTGTCAGTGTCTGCTCTCAC
CTTGCCAAAGACTACCTCCCTTCCCTCTGTCAGGCCGACGCGAGGAGGACGCTGGGTGAT
GGTGATTCTGCCTCGCATCCCAACCGAGGACTGAGGAACCTAGAGGGGACCTCCGGGC
CTGGGCTGCCCTCTGATGCTCGCCCTGATTTTCTTCATCTCCAGTTCTGGACAGTGCAG
GTGGCAAGAAAAGGCGCTAGTTTAGGCTATGCCCTGGAGATGAATTATGAGGCTCAA
GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTCTC
AGGCTGAGGGGGGAACATTTTGTGTGATATAAATACCTAAATCGACTCTTTTTTCTTTTT
GAGGTGGGGGGAGGAGGAGGATATATGGAATCTTCTAACCTCTTGGGCTATATTTTCTC
TCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTGCTGCCCTTCTCTTGGTCCCAGACCTT
GGGGGAAAGGAAGGAGGTGCATGTTTGGGAGACTGCCATTACTGGAATCAATGTTTAACTCT
CCTTAACACACGACATCTCTCTCTCCCAAGGTGAGTGAGGAGGCTGCTGTGGTGAAGTGGC
CACTCCAGAGTGCAGTTGCCACTGGAGGAGTCAGACTACCATACCATGAGTCTGAGGAGGAGGG
GAGATTTTGTGAGTTTAAATTTGGGCTGTGGGAGGGGGGAGGTTTCTATAAAGTGT
ATCATTTTCTGCTGAGGGTGGAGTGTCCCATCTTTTAATCAAGGTGATTGTGATTTGACT
ATAAAAAAAGAAATTTGTAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 220

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVWVFILVHVTDR
SDARLQYGLLI FGAAVSVLLQEVFRFAYYKLLKKADEGLASLEDGRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIHGDSPIYFLTSAFLTAAILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

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FIGURE 221

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
TCACCCATTANTTCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

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 $\frac{p_{89}}{p_{90}}$
 $\frac{p_{91}}{p_{92}}$
 $\frac{p_{93}}{p_{94}}$
 $\frac{p_{95}}{p_{96}}$
 $\frac{p_{97}}{p_{98}}$
 $\frac{p_{99}}{p_{100}}$

FIGURE 222

GACCGACCGTTCAGATGCCCGGTTCCAGTACGGCTTCCTGATTTTTGGTGCTGCTGNTCTG
TCCTTCTACAGGAGGTGTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTTNTCTGTTATCAATATTTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCATTAAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA
GAGGAG

FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCTTTCCTTTCCCCG
GGGTCTGGGGTGACATTGCACGGGCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCTTCCCACNTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACCTTCGTCGCGTTCGGCCCGGCCCTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGAGGGGCA
TTTTTCTGGCTGGTCTCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
CGACCGGTCAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTGGTGCTGCTGTCTGTCC
TTCTACAGGAGGTGTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCTCCCTTTCCCNNTCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCCCTCCCATTTGCCCTGTCTGGTCAGGCCCCACCCCCCTTCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACCTTCGTCGCGTTCGGGCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGC
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA
CCGACCGGTCAGATGCCCCGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTC
CTTCTACAGGAGGTGTCCGCTTTGCCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGTCTGTGCGTCTGCAACCCACATCTTTCTCTGTCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCTATAGTGCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CTTGTGGTTCTCTCTACCTGGGGAATAAGGTGCAGCGGCC**AT**GGCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTCACAGAGCATGTT
 CTCGCCAACAAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGCGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCAAC
 CAGCTCTACTGCGGGCGGTGTGGTGATCCACAGTGGCTGCTCACGGCCGCCACTGCGAG
 GAAGAAAGTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTACCAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCTGGCTACTCCCACCTGGCCACTCT
 AACGACCTCATGCTCATCAAATGAACAGAAGAATTGCTCCCACTAAAGATGTCAGACCCAT
 CAACGTCTCCTCTCATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA
 CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGTCTTGGGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCC**TG**AGTCAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTTCAG
 ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTTACTCTCTCCAGCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCTGG
 GAACAAATTTCCAAAAGTGTCCAGGGCGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA
 CTGAGAAAGTGAAAAA

FIGURE 226

MATARPPMWMVLCALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSI PHPGYSHPGHSNDLMLIKLNRRI RPTKDVRP INVSSHCP SAGTKCL
VSGWGTTKSPQVHFVKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGRDSCQGDSGGP
VVCNGSLQGLVSWGDP CARPNRPGVYTNLCKFTKWIQETIQANS

FIGURE 227

ATGGTCAACGACCGGTGGAAGACCATGGGCGGCGCTGCCAACTTGAGGACCGGCCGCGCGA
 CAAAGCCGACCGGCGGAGCTCGGGCTACGTGCTGTGCACCGTGTCTGCTGCCCTGGCTGTGCT
 TGGCTGGCTGTAGCTGTACCGGTGCCGTGCTCTTCTGAACACGCCACGCCGCGCGGACG
 GCGCCCCCACTGTCTGCTAGCACTGGGGCTGCCAGCGCCAACAGCGCCCTGGTCACTGTGGA
 AAGGGCGGACAGCTCGCACCTCAGCATCCTCATTTGACCGCGCTGCCCGACCTCACCGACA
 GCTTTCGACGCGCTGGAGAGCGCCAGGCCCTCGGTGCTCGAGCGCTGACAGCGCCACAGGCC
 GACCCACGGCTGGTGGGGCAGCAGGAGCAGGAGTGCTGGACAGCTGGCCAGCAGCTGCC
 CCGGCTGCTGGCCCGAGCCTCAGAGCTGCAGACGAGTGATGAGGGCTGCGGAAGGGGCATG
 GCACGCTGGGCGAGGCCCTCAGCGCCCTGCAGAGTGAGCAGGGCGCCCTCATCCAGCTTCTC
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACCTCCGTGAGCGACATCTCGGATGCCCT
 GCAGAGGGACCGGGGCGCTGGGCGGGCCCCGCAACAAGGCCGACCTTCAGAGAGCGCCCTGCC
 GGGGAACCCGCGCCCGGGGCTGTGCCACTGGCTCCCGGCCCGAGACTGTCTGGACGTCTCTC
 CTAAGCGGACAGCAGGACGATGGCGTCTACTCTGTCTTCCACCCCACTACCCGGCCGGCTT
 CCAGGTCTACTGTGACATGCGCAGGACGCGCGGGGCTGGAGGCTTTTCAGCGCCGGGAGG
 ACGGCTCCGTGAACCTTCTTCCGGGGCTGGGACGCGTACCAGAGACGGCTTGGCAGGCTCAC
 GGGGAGCACTGGCTAGGGCTCAAGAGGATCCAGGCCCTGACCACACAGGCTGCCACGAGCT
 GCACGTGGACCTGGAGGACTTGAAGATGGCAGCGCCTATGCCCGTACGGGAGCTTCGGG
 TGGGCTTGTTCCTGCGACCTTGAGGAAGACGGGTACCCGCTCACCGTGGCTGACTATTCC
 GGCACCTGCAGGCGACTCCCTCTGAAGCAGCGGCGATGAGGTTACACCACAGGACCGTGA
 CAGCGACCATTCAGAAACAACTGTGCCGCTTCTACCGCGGTGCCGTGTGTACCGCAACT
 GGCACAGCTCAACCTCAATGGGCAGTACCTGCGCGGTGCCACGCGCTCTATGCGGACGCG
 GTGGAGTGGTCTCTTGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG
 GCGGTCGGGAGGACCG**TAG**ACTGGTGCACTTGTCTTGGCCCTGGCTGGTCCCTGTGCC
 CCCATCCCCACCCCACTCACTCTTTCGTGAATGTTCTTCCACCCACTGTGGCTGGCGGAC
 CCACTCTCCAGTAGGGAGGGGCCGGGCCATCCCTGACACGAAGCTCCCTGGGCGGTGAAGT
 CACACATCGGCTCTCGCGCTCCCCACCCCTCCATTTGGCAGCTCACTGACTCTCTTGCCTC
 TGCTGATGGGGGCTGGCAAACCTTGACGACCCCACTCCTGCTGCCCTGACCTGTGACTCCGG
 TGCTGTTTGGCGTCCCCTGGCCAGGATGGTGGAGTCTGCCCGAGGACCCCTCTGCCCTGCC
 GGCAAATACCGGCAATTATGGGGACAGAGAGCAGGGGCGACAGCAGCCCTCGGATCTCTC
 CTAGCAGATCGTGGGGAATGTGAGGTCTCTCTGAGGTGAGGTCTGAGGGCAGTATCTCCAG
 CCTCCGAATGCCAACCCCAACCCGTTTCCCTGGTGCCACAGAGAACCACCTCTCCCCAA
 GGGCCTCAGCTGGCTGTGGGTGGGTGGCCCCATCTTACCAGGCCCTGAGGTGAGGATGGG
 GAGCTGCTGCTTTTGGGGACCCACGCTCCAAGGCTGAGACCAATTCCTTGGAGGCCACCCAC
 CCTGTGCCCGGCGAGGCTGGGGTCTGCAGTCTCTTACCTGTCTGTGCCACCTGTCTCTGT
 TCTCAAATGAGGGCCCAACCCATCCCCACCCAGCTCCCGGCCGTCTCTACCTGAGCGCAGC
 CGGGGCTGCCATCCATTCTCTGCTCTTGGAAGGTGGGTGGGGCCCTGCACCGTGGGGCT
 GGAATGCGCTAATGGGAAGCTCTTGGTTTCTTGGGCTGGGGCCCTAGGCAGGGCTGGGATGAG
 GCTTGTACAACCCCAACCAATTTCCAGGGACTCTCAGGGTCTTGGAGCCTCCCAAGGAGG
 GCTTGGGGGTGATGACCCCTTCCCTGAGGTGGCTGCTCCATGAGGAGGCCAACCCCTGCC
 ATTGACCTGGGCCACTGGACCCAGGCCAGGCCCGGGCCCGGCGAGTGGTCAAGGGACAGGGA
 CCACCTCAGCGGCCAAATGGGGTGGGGGGAAGTGGGGCAGCACAAGGCCAGCCACTGGACA
 CTTTCTTGTGTAATCTTCCCAACCCAGCAGCTGTCAATCCCCACTCTTGTGTGACACA
 TGCAGGCTGAGACCCGAGGCTCCAGGACCAAGCAGCACAAGGCCAGGGCTGGAGCGCGGG
 TCCTCAGCTGTCTGCTCAGCAGCCCTGGACCCGCGTGCCTTACGTCAGGCCAGATGACAGG
 CGGCTTTTCCAAGGCTCTCTGATGGGGGCTCCGAAAAGGCTGGAGTCAGCCTTGGGAGCT
 GCTTACGAGCTCTCTCTGGGACGAGGGGAGGTGGCTCTCTCAAAGGACACCCGATGGCA
 GGTGCCATGGGGGTGGGGGTTCCGTTCTCCCTTCCCTCCCACTGAAGTTTGTGCTTAAAA
 AACAATAAATTTGACTTGGCACCCTGGGGGTGGTGGGAGAGGGCGTGTGACCTGGCTCTC
 TGTCAGTGCCACCGGTCACTCCACATGGCGAG

FIGURE 228

MVNDRWKTMGGAAQLEDPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQLLDTLADQLPRLARASELQTECMGLRKHGHTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAVELHVDLEDFENGTAARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

FIGURE 229

GCAGTCAGAGACTTCCCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT
 TGCTTCTCTGAAGTACTAGCTACAGTAGCCCGCGGCCAGGGCAATCCGACCACATTTCACTCT
 CACCGCTGTAGGAATCCAGATGAGGCCAAGTACAGCAGCAGGAGCATGCTGGATGATG
 ATGGGGACACACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGAC
 TTTGTGCTTGGTGTCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTCCTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTTCTCAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC
 TGAATAACTCTGTCTGTGAGCTGTATAACAAAGCTGGAGCACACAGTGCAGCCCTTGTACAG
 AACAATGGAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTTCTGCCTTAGTGAAACTCTACCATGCTGAAGATAAACAACAAGAAGA
 CCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTATTGGACAGGGCTTT
 TGCGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTG
 TTCCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACATGATTCGCC
 CTCTGCAACTACAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
 TGGGAATGGAACATAATCAGGAAAGACTATCTCTGACTAGTACAAAATGGGTCTCTGTG
 TTTCTCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCAGTATTTAACAGTACAA
 AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTCTATCTGCCTTCTTG
 GCTTAGAGATAACTTTTAGCTCTCTTTCTCTCAATGTCTAATATCACCTCCCTGTTTTCAT
 GTCTTCTTACACTTGGTGAATAAGAAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACC
 AGCAAATACACAAGGAATCTTTTTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCAT
 CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCCTTCTGTGTCCATTAAAGCTCTGATAATTG
 TCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCCGATATTCCTTTCAGAGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCA
 TCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTTCAG
 GTACTGAAGATTTAATAATAATAAATGTAATACTGTGAAAAA

FIGURE 230

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSSTWRPVALTLLTLCVLVL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDGKAWLWMDGTPFTSELFHIIIDVTSRPSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

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FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGNTCCTTTTCAACGTGGCGACCAGTGGCCCTGACCCCTG
CTGACTTTGTGCTTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAGAGTTGCAATTNTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTNTGCAGCAT
GTGGCTGAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACCTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC

FIGURE 232

GCCGAGCGCAAGAACCCTGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CGGGGATTTCGGCTCGGGCCGCTGGGCTCTGCTCTGCGGGGAGGAGGCGGGGCCCGCGGGG
 CCCGAGCCCTCCGGATCCGCCCCCTCCCGGGTCCCGCCCTCGGAGACTCTCTTGCTGCT
 CTGGGGGTTCCGCGGGGCGGGGACCCGCGGTCCGGGCGCC**ATG**CGGGGCATCGCTGCTGCTG
 TCGGTTGCTCGGGCCCGCAGGGCCCCGTGGCCGTGGGCATCTCCCTGGGGTTACCCCTGAGCCT
 GCTCAGCGTCACTTGGGTGGAGGAGCGCTGCGGCCACGGCCCGCCCAACCTGGAGACTCTG
 AGTGCGCGCGCGCGGCAACACCAACGCGCGCGCGCGGCCCAACTCGGTGCAGCCCGGAGCG
 GAGCGCGAGAAGCCCGGGGCGCGGCAAGCGCGCGGGGAGAATTGGGAGCCCGCGCTTCTGCC
 CTACCACCCTGCACAGCCCGCGCAGCGCCCAAAAAGGCCGTGAGGACCCGCTACATCAGCA
 CGGAGCTGGGCATCAGGCAGAGCTGCTGGTGGCGGTGCTGACCTCTCAGACCACGCTGCC
 ACGCTGGCGGTGGCGCTGAACCGCACGCTGGGGCACCGGCTGGAGCGTGTGGTGTCTCTGAC
 GGGCGCACGGGGCGCGCGGGCCCACTGGCATGGCAGTGGTGACCTCGGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACCACTTTGAC
 TGGTTCTTCTTGGTGCCTGACACCACCTACACGAGGGCGCACGGCTGGCAGCGCTTAACCTGG
 CCACCTCAGCCTGGCTCCGCGGCCACCTGTACCTGGGCGGGCCCCAGGACTTCATCGGGC
 GAGAGCCCAACCCCGGCCGCTACTGCCACGGAGGCTTTGGGGTGTGCTGTCCGCGCATGCTG
 CTGCAACAACCTGGCGCCCACTTGGAGGCTGCGCGAACGACATCTGCTAGTGGCGCGCCCTGA
 CGAGTGGCTGGGTGCTGCTGCTGCTGATGCCACCGGGTGGGTGCACTGGTGACCAGGAGG
 GGGTGCCTATAGCCATCTGGAGCTGAGCGCTGGGAGGCCAGTGACGAGGGGGACCCCTCAT
 TTCCGAAGTGGCTTGACGCGCCACCTGTGGCTGACCTGTGACACATGTACCAGCTGCACAA
 AGCTTTCCGCCCGAGCTGAACCTGGAACGCACGTAACAGGAGATCCAGGAGATTACAGTGGGAGA
 TCCAGAATACCAACCATCTGGCCGTTGATGGGGACCGGGCAGCTGGTTGGCCCGTGGGTATT
 CCAGCACCATCCCGCCCGGCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCA
 GCACGCTTTCTCCTGCGCGCATGGCTCACCCCGCTGCCACTGCGGTGGGGCTGACCCGGGCTG
 ATGTGGCGGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCGCTACCAACCGGGCTTG
 CGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCCGGGGTATGGA
 ATACACGCTGGACTTGCAGCTGGAGGCACTGACCCCCAGGAGGCCCGCGGCCCTCACTC
 GCCGAGTGCGAGCTGCTCCGGCCGCTGAGCCGCGTGGAGATCTTGCTGTGCCCTATGTCACT
 GAGGCTCACGCTCTCACTGTGCTGCTGCTGCTTCTAGCTGCGGCTGAGCGTGACCTGGCCCTTG
 CTTCTTGAGGCGCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGGCTGACCC
 TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCTGGCCATGCAGATGTCTTCGACCT
 GTCAGGCCACAGTGGCAGAGCTGGAGCGGCGTTTCCCGGTTGCCGGGTGCCATGGCTCAG
 TGTGCAGACAGCCGCACTCACCACTGCGGCTCATGGATCTACTCTCCAAGAAGCACCCGCG
 TGGACACACTGTTCTGCTGGCGGGCCAGACAGGCTGCTCAGCGCTGACTTCTGAAACCGC
 TGCGCGATGCTATGCGCATCTCCGCTGGCAGGCTTCTTTCCCATGATTTCCAAGCCTTCCA
 CCCAGGTGTGGCCCCACCACAAGGGCTGGGCCCCAGAGCTGGGCGTGACACTGGCCGCT
 TTGATCGCCAGGCAGCCAGCGAGGCTGCTTCTACAACCTCGACTACGTGGCGGCCGCTGGG
 CGCTGCGCGAGCCTCAGAACAAGAAGAGGAGCTGCTGGAGAGCCTGGATGTGTACGAGCT
 GTTCTTCCACTTCTCAGTCTGCATGTGCTGCGGGCGGTGGAGCCGCGCTGCTGCAGCGCT
 ACCGCCCCAGAGCTGCAGCGCGAGGCTCAGTGAGGACCTGTACCACCGCTGCCCTCCAGAGC
 GTGCTTGAGGGCCTCGGCTCCCAACCCAGCTGGCCATGCTACTCTTTGAACAGGAGCAGGG
 CAACAGCACCT**G**ACCCCACTCTGCCGCTGGGCGTGGCGCACACCCCAACCCCACTT
 CTCCCCCAAAACAGAGCACTGCGAGCCTGCTGGGAGGGCTGGCCGTAGCCAGACCC
 AAGCTGGCCCACTGGTCCCTCTGTGGCTCTGTGGTCCCTGGGCTCTGGACAGCACTGGG
 GGAGCTGGCCCCAGAGCCACCCACTTCTCATCCAAACCCAGTTTCCCTGGCCCTGAGCCT
 GCTGATTCGGGCTGTGGCTTCCAGCTATTTATGCACTACAGCTGAGCTGACCGCCAGCCTGC
 CTCTGGGCGCTGGGGCTGGGCTGTAGAAGTGTGTGGGAGAGGAGGAGCTGAGGAGGGG
 GCATCTCCCAACTTCTCCCTTTTGAGACCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCA
 AGTGTGGAAAAA

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQRLLVAVL
TSQTTLPTLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLLLE
QHGDDEFWFFLVPDTTYTEAHGLARLTGHLSSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPEDEWLGRCILDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFERSALTAHFVRDPVHMYQLHKAFARAELEPTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLTALAEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPOGGRRLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPRLMDLLSKKHPLDTLFLLAGPDTVL
TPDFLNRCRMHAISGWQAFPPMHFQAFHPGVAPPQGGPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLHVLRAVEFALLQRYRAQTC SARLSEDL
YHRCLQSVLEGLGSRTQLAMLLFEQE QGNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCAACGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTCGGCAGGGCCCGCTTTTGTAGAAGCTTGATTTCCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTACCGATTCTTCCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG
 AGGGTTGCTCAACGCCCCGCTCATTGGAAAACCAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT
 TTCCCCGCCCTGAGACCCTGCAGCACCATCTGTC**ATGG**CGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCGCTCTTTGGCGGCAGCGGCAGCGAGGGCTCCCGCCGCCCGCTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGAAAGCGGCCCCAGAAC
 CGACCACACCGTGGCAAGAGGCCCAAGACCCGAGGACGAAAACCTGTATGAGAAGAACCCA
 GACTCCCATGGTTATGACAAGGACCCGTTTTGGACGCTCTGGAACATGCACCTTGTCTTCTT
 CTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACCTTTGTGGCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC
 CTTCCCATCATGGAATCCAATGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCAGCGAGGGC
TCCCGGCCGCCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAGCGGCCCCAGAACCACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAACCTTGATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG
TCTGGAACATGCGACTTGCTTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAACCTGCTTCGACCCAGCA
AGATCCAG

FIGURE 237

GCGGCGGCT**ATG**CCGCTTGCTCTGCTCGTCTGCTCTGGGGCCCGCGGCTGGTGCCT
 TGCAGAAACCCACGCGACAGCCTGCGGGAGGAACTGTGCATACCCCGCTGCCTTCCGGGG
 ACGTAGCCGCCACATTCCAGTCCGCACGCGCTGGGATTCCGAGCTTCAGCGGGAAGGAGTG
 TCCCATACAGGCTCTTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCATTACACAAGGCTTTTGGAGACCCGATCTGGGGGCCACCCCTTCTCTGC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAA
 TCTTGGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCTCTCTCAACTTCATCGA
 CTCCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAACCTCACC
 CCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCCACACAGCTACCACTCCCAAGGCAGTGCATATCCGCCCTGTTTGCAGAAATG
 CACGCTGTACTAGCATCTCTGGGAGCTGAGGCAGACCCTGTCACTGTGATTTGATGCCTTC
 ATCAGGGGCGAGGAAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCCCTCACGGA
 GCCCTGCCCTTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACCTACAACACAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGACGTCATCTTAGGCACT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACTCTCGAAACCT
 CAACATCCAGCTCAAGTGAAGAGACCCCGAGAAATGAGGCCCCCACTGGCCCTTCTCTGC
 ATGCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAGGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCGGGCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGGG
 GCTGTATGTGCACACCTCACCATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC
 ACTACCAGCTGCCAGGACCGGCTGCAACCCACCTCTGGAGATGCTGATTGAGTGGCG
 GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGCACCGAGTA
 CACGCCAGATCTTAACATGGCTTCTATGTACGCCCATCTGCTCAGCGCCCTTGTGGCCCA
 GCATGTAGCAGCAAGCCAGTGGACTGGGAAGAGATCCCTCTTCAACAGCCTGTTCCTCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCAGTGCAGTGTGGTGGCGGTGT
 GCTACGGCTCCTTCTACAATCTCTCACCCGAACCTTCCACATCGAGGAGCCCCGCACAGGT
 GGCTTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCCGAGGTGTCCCCCACT**CTGA**TT
 CTTGCCCTTTCCAGCAGTGCAGCTGCCGTTTCTCTCTGGGGAGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTCCCTGGACAGGTCAAGGC
 CTACAGCTGTGTTGCCAGTACAGGAGCCACGACCCAAATGTGGCATTTGAATTTGAATTA
 CTTAGAAATTCATTTCCTACCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGGTCGGTGGCTGCTATTGGACAGCACAGAAAAAGATTTCCATCACCACAGAAAGGTC
 GGCTGGCAGCACTGGCCAAAGGTGATGGGGTGTGCTACACAGTGTATGTCAGTGTGTAGTGA
 TGGAGTTTACTGTTTGTGGAATAAAAACGGCTGTTTCCGTGGAATAAAAAAAA

FIGURE 238

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPAKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDTVTDVDKSWK
ELSNVLSGIFCASLNFIDSTNTVTPTASFVKPLGLANDTHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRARCTSSISWELRQTLVSVFDAFITG
QGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPPEEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTPWYLRLYVHTLTITSGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSIQFERALLKWTEYTPDPNHGFIYVSPSVLSALVPSMVAAPVDWEESPLFNSLFFVSD
GSNYFVRLYTEPLLVLNLTPTDFSMYPNVICLTCTVVAVCYGSFYNNLLTRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCAAGTGTACACAGACCAAGGACTGTCTGGGGGAAAGGAAGTG
TTGTTACCTGCACGTGTGGCTTCAAGTGTGTGATTCCTGTGAAGGAAGTGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCCTCAGAAATGATGCTGGGTCCCTTCTACCTCTGGGGGTCACTC
TCACCTTGGCACCTGCCCTGAGGGTCCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC
CCACCAAGAAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAAGAGGGAAGAGTCACAAAAAG
TCCAGACCCCAAGGACGGTACTTCCCTCTCTACCTGGTGTCTCCTTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAAGTGCCTTATAAGAGACCCCAAGAGCTGCCTTGCCTTC
TGCAATGTGTGATCAGCTAGAAGGCACGTGTGAGAGAAGAGAACTGGTCCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGGACTTCCAGCCTCTAGAACTGTAAGAAATAAATAT
TTGCTGTTTATAATCCAA

FIGURE 240

MGSSSFLVLMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
 YLHCGFKCVIPVKELEEKGKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

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FIGURE 241

AAACCTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCTTGCCAGG
 AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCCGACCCACCACCA**ATG**AGGTCCTGCCTGTGGAGATGCAGGCACCTGAGCCAAAGG
 CGTCCAGTGGTCTTGCCTTCTGGCTGTCCGTGCTTCTTCTCTTCCGCTTGCCCTCTTTTA
 TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAGAAAGGTCT
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA
 TGCAGAGCCAGCGCCAGAGAACATGCCCTCAACACACAAACCCAGCCCAAGGCCACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACCAGGCACCGCCGAGGAGCAGGCAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCCCAGAAAAAGAGAAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAAGACGACCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG
 GTGTGAGAGAAGCACCAGGGCAAAGCGGCAACCACAGCCAAGACGCTCATTTCCAAAAGTCA
 GCACAGAAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCATCCCACTAAGGAGAAGAACTCAGGCCACCCCAACCCCTGCCCCCTTTCCAG
 AGCCCCACGACGCAGAGAAACCAAGACTGAAGGCCGCCAACTTCAAAATCTGAGCCTCGGTG
 GGAATTTTGAAGAAAAATACAGCTTCGAAATAGGAGGCCACTCAGACGACTTGCCTGACTCTG
 TGAAGATCAAGCCTCCAAGTCGCTGTGGCTCCAGAACTCTTTCTGCCAACCTCACTCTC
 TTCTTGAGCTCCAGACACTTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTTGCACCACC
 CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGCAGAAAGTCGTGACACGCTTCCCTCCAG
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCGCTGGGAGCCTCCGGTGATCACCTGT
 GCCGTGTTGGGCAACGGGGGCATCTGAACAACTCCACATGGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGGACTC
 GGACATCCTTCTACGGCTTACCGCCTTCTCCCTGACCCAGTCACTCCCTATATTTGGGCAAT
 CGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCGCTACTTGCACCTTCTGGAAGGCAC
 CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT
 TCTGGTTCAGGCACAGACCCAGGAAGCTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG
 TTGCTGCACCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCCCTGGA
 TGGTGCCCACTGGAGGATATACGCCCCACCAGTGGGGCCCTCCTGCTGCTCACTGCCCTTC
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGCTTGGAAAGCGCTACACGATGAAGGGATAATCCGGCTGTACCAGCGCTCCTGGTC
 CCGGAACCTGCCAAAGCCAGAAGCT**CGA**CGGGGCCAGGGCTGCCATGGTCTCCTTGCCCTGCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCCATGGGCTCAGACTAA
 GCTCCAAGCCCTTCAGGAGTTCGAAGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAAATGGCTAAATTGAGGTTCTGAAGTCTTTCAGTACATTGCTGTAGGTCTTGAGGCCAGG
 GATTTTAAATTAATGGGGTGATGGGTGGCCAAATACCAAACTTCTGCTGAAAAACACTCTT
 CCAGTCCAAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGATCTG
 GTTTGAATTCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTAACTTCACTAC
 AGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTTAGAAAGGCTTATACTTGTCTTG
 TCTTTAAGCTATTTGACAACTTACGTGTTGTAGAAAACCTGATAATAATACAAATGATGTT
 GTCATGGAAGGCAATAAATTTTCTACAGTGAAAAA

FIGURE 242

MRSCLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP
 KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQNGGGQTRKLTASRTVSEKHQG
 KAATTAKTLIPKSHRMLAPTGAVSTRTRQKGVTAVIPPEKKKPQATPPPAPFQSPTQRN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKFLPNLTLFLDSRHF
 NQSEWDRLEHFAPPPGFMEELNYSLVQKVVTFRPPVPQQQLLLASLPAGSLRCITCAVVGNGG
 ILNNSHMQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATFSLTQSLILGNRGFKNVP
 LGKDVRYLHFLEGRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLHLPDFL
 RYMKNRFLRSKTLGDAHWRIRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYDTSW
 KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAACACTTCCATAGACTTTATCACACA
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCCATGG
ACAAGAGATTTATTTTGCAGACAGACTCTTCCATAAGTCCTTTGAGTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATTT

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FIGURE 244

MRGPGHPLLGLLLVLGSPSEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

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FIGURE 245

GGGCTGGGCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCTCGCGTCCCTTCTCTGGGAGG
CCCGACCCCGGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGCGCCG
CTCACCGCAATCGCTCTGTTGGTCTGGGGGCTCCCTGGTCTGGCCGGCGAGGACTGCCT
GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTCACCTTCT
GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTTGCTACCTGT
ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGATTCCAATGACAGGCATC
CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCAAAGCTGGCCCTGCACCCCCACAGCC
TGGCTTCATGTACCCACCTAGTGGTCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
CAGTCTACAACCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGGAACCAGCCATGTCTCTGCTGCCCTTCAGTGATGCCAACCTTGGGAGATGCCTCAT
CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCTCCAGCCACCAGGCCCCAGACCAA
GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGGAAACAGGAGCTGAAGTAGA
ACTATGAGGGGTGGGGGGAGGGCTTGAATTATGGGCTATTTTACTGGGGGCAAGGGAGG
GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAGATCCCAG
CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT
TCCGTGAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCACTGGCCACATCTCTGGCCTG
CTAGATTAAAGCTGTAAGACAAAA

FIGURE 246

MPPAGLRRAAFLTAIALLVLGAPLVLAGEDCLWYLDNRGSHWPGFNCEFFTCCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYQDPKAGPAPPQPGFMYPPSGPAPQYPLYAGPPVYNPAAPPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

FIGURE 247

GGGGGAGCTAGGCCGGCGCAGTGGTGGTGGCGCGCGCAAGGGTGAGGGCGGCCCGAGAA
 CCCCAGGTAGGTAGAGCAGAAAGATGGTGTCTTCTGCCCTCAAATGGTCCCTTGCAACCATG
 TCAATTTCTACTTTCTCTACTGTTGGCTCTCTTAACTGTGTCCACTTCTCATGGTGTGCAGAG
 CACTGAAGACTCTCCAAAACGCTAGTGTAGGGACACCATTTCTTGGAAATAAAATACGACTTC
 CTGAGTACGGTCATCCGAGTTCATTATGATCTTGTATCCATGCAAACTTTACCACGGTGACC
 TTCTGGGGAGCCACGAAAAGTAAAAATCACAGCCAGTCAGGCCACAGCACCATTCACTCTGCA
 TAGTCACCACTGCAGATATCTAGGGCCACCCTCAGGAGGCAATTTGCACCTGTCTGGCTCCCGAG
 AAGAACCCTTGCAGGCTCTGGGAACCCCTCAGGAGCAATTTGCACCTGTCTGGCTCCCGAG
 CCCCCTCTGTCTGGGCTCCCGTACACAGTTGTCTTCACTATGCTGGCAATCTTTGGGAGAC
 TTTTCCAGTGATTTTACAAAAGCACCTACAGAACCAGGAAGGGGAACTGAGGATACCTAGCAT
 CAACACAATTTGAACCCACTGCAGCTAGAAATGGCCTTTCCCTGCTTTGATGAACCTGCCTTC
 AAGCAAGATTTCTCAATCAAAATAGAAGAGAGCCAAAGGCACCTAGCCATCTCCAATATGCC
 ATTGGTGAATCTCTGACTGTTTCTGAAGGACTCATAGAAGCACCATTTTGATGTCACTGTGA
 AGATGAGCACCTATCTGGTGGCCTTTCATCTATTGAGTCTGTGAGCAAGATAACC
 AAGAGTGGAGTCAAGGTTTCTGTTTATGCTGTGGCCAGACAAGATAAATCAAGCAGATTATGC
 ACTGGATGCTGGGCTGACTCTTCTAGAAATTTATGAGGATTTTTCAGCATACCGTATCCCC
 TAGCCAAACAGATCTTCTGCTGCTATTCGGACTTTCACTGTGGTGTATGGAAAACCTGGGGA
 CTGACAACTATAGAAATCTGCTCTGTTGTTGATGCAGAAAAGCTTCTTCTGCATCAAGATAA
 GCTTGGCATCAGTGAAGTGTGGCCCATGAACCTGGCCACAGCTGTTTGGGAACCTGGTGA
 CTATGGAATGGTGAATGATCTTTGTGCTAAATGAAGGATTTGCCAAATTTGAGGATTTGTG
 TCTGTGAGTGTGACCATCTCTGAACCTGGAAGATTATTTTGGCAATGTTTTGA
 CGCAATGGAGTGAATGCTTTAAATTCCTCACACCCTGTGTACACCTGTGGAAAATCCCTG
 CTCAGATCCCGGGAGTGTGTTGATGATGTTTCTTATGATAAGGGAGCTTGATTTCTGAATATG
 CTAAGGGAGTATCTTAGCGCTGACGCAATTTAAAAGTGGTATTTGTACAGTATCTCCAGAAGCA
 TAGCTATAAAAATACAAAACAGGACCTGTGGGATAGTATGGCAAGTATTTGCCCTACAG
 ATGGTGTAAAAGGGTGGATGGCTTTTGTCTAGAAGTCAACATTCATCTTCATCCCTCACAT
 TGGCATCTGAGAGGGGTGGATGTGAAAACCATGATGAACCTTGGACACTGTCAGGAGGGGTTT
 TCCCTATATAACCATCAGATGAGGGGGAGGAATGTACACATGAAGCAAGAGCACTACATGA
 AGGCTCTGACGGGCCCGCCGACACTGGGTACCTGTGGCATTTCCATGACATTCATCACC
 AGCAAAATCCAACATGGTCCATCGATTTTGTCTAAAAACAAAACAGATGTGCTCATCTCTCC
 AAGTATGAGTGAATGGATGATTTAATGTGGGCATGAATGGCTATTACATTTGTCATTACG
 AGGATGATGGATGGGACTCTTTGACTGGCCTTTTAAAAGGAACACACACAGCAGTCAAGCAT
 AATGATCGGGCAAGTCTCATTAAACATGCAATTTCACTCGTCAGCATTTGGGAAGCTGTCCAT
 TGAAGAGCCCTTGGATTTATCCCTGTACTTGAACATGAACTGAAATTTAGCCCGTGTGTTT
 AAGTTTGAATGAGCTGATTTCTATGTATAAGTTAATGGAGAAAAGAGATATGAATGAAGT
 GAAACTCAATTCAGGCCCTTCTCATCAGGCTGCTAAGGGAGCTCATGTATGAAGCAGACATG
 GCAGAGCAGGGGCTCAGTCTGCAGAGCAAAATGCTGCGGAGTGAACACTACTCTCTCGCTGTG
 TGCACAACATTCAGCGCTGCGTACAGAGGGCAGAGGCTATTTTCAGAAAAGTGGGAAGGAATCC
 AATGGAAACTTGAAGCTGCTGCTGCAGCTGACCTTGGCAGTGTGTTCTGTGGGGGCCAGAG
 CACAGAAGGCTGGGATTTTCTTTATAGTAAATATCAGTTTCTTTGTCCAGTACTGAGAAAA
 CGCAAAATTTGAAATTTGCCCTCTGCAGAACCCAAAATAAGGAAAAGCTTCAATGGCTACTAGAT
 GAAAGCTTTAAGGGAGATAAAATAAAACCTGAGGATTTCCACAATCTTTACACTCATTTGG
 CAGGAACCCAGTAGGATAGGCTAGCCACTGGCCTCAGCAATTTCTGAGGAAAACCTGGAACAACTTG
 TACAAAAGTTTGAACCTTGCTCATCTTCCATAGCCACATGGTAAATGGGTACAACAATCAA
 TTTCTCAACGAACACGGCTTGAAGAGTAAAAGGATTTCTTCAAGAGCTTGAACGATGTA
 TTTCTCAGCTCGGTTGTGTCCAACAGACAATTTGAACCATTTGAAGAAAACATCGGTGGATGG
 ATAGAAGTTTTGTATAAATGCAGAGTGTGGCTGCAAGTGAAGAGCTTGAACGATGTA
 TTTCTCCCTTGCCCGGTTCTGTTATCTCTAATCACCACATTTTGTGAGTGTATTTTCAA
 ACTAGAGTATGGCTGTTTTGGCTTCAACTGGAGTACTTTTTTCCCTTCAACTCATTTTGA
 CTATCCCTGTGAAAAGAATAGCTGTAGTTTTCATGAATGGGCTTTTCATGAATGGGCTGA
 TCGCTACCATGTGTTTTGTTTCTATCACAGGTGTGGCCTGCAACGTAACCAAGCTGTTGGGT
 TCCCTGCCACAGAAGAATAAAGTACTTATTCTTCTCAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
 YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLOVLE
 HPPQEQIALLAPEPLLVLGPYTVVIHYAGNLSETFHGFKYSTYRTKEGELRILASTQFEPTA
 ARMAFPCFDEPAFKASF I KIRREPRHLAISNMPLVKS SVTVAEGLIEDHFDVTVKMSTYLVA
 FIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLFEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVVAHELAHQWFGNLVTMEWWNDL
 WLNNEGFAKFMFVSVSVTHPELKVG DYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGM DG
 FCSRSQHSSSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVHRFLKTKTDVLILPEEVEWIKFNVGMNGYIIVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLVSI GKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
 MYKLMEKRD MNEVETQFKAFILRLRLDLIDKQTTWDEGVSVEQMLRSELLLLACVHNYQPCV
 QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSSTEKSQIEFALC
 RTQNKELQLWLLDESFKGDKIKTQEFFQILTLIGRNPVGYPLAWQFLRKNWNKLVQKFELGS
 SSIAHVMVGTNNQFSTRTRLEEVKGGFSSSLKENGSQLRCVQQTIEETIENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTC**ATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
 TGCCAGGAGTGACAGCGCTGCTCTGCCAGTTTGGGACAGTTGAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
 CACGTTGATGCTCATTTAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGACCACACACTGTTATGAT
 GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTTCTGACCTGTCTCGGGGACCACCATTATGACACACGGAAAC
 TTGGCTCAAGAACCCTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGCGAGGT
 GTGTGACGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGACAAAAG
 GCTGACGACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCTCCTGGG
 GTGCTTGTGGCCTCCTATACCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTCT
 CTACCTGTGTGACGCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GGCGCCACTCATTGTTATGATGGGTACATTATCTCTCAGGAGGTGGGCTGTCCACCAAAAT
 GAGCATTGAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGTAACACACACAGACAATCG
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGACGCTCCTGCTCCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTTGCCTTCTGCT**TAA**CTCTATTACCCCCACGATTCTTACCGCTGCTGA
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTTC
 CCATTCTGTCCATGAATCATCTTCCCCACACAATCATTCATATCTACTCACCTAACAGCA
 ACATGGGGAGAGCCTGGAGCATCCGACTTGCCTATGGGAGAGGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

FIGURE 250

MSAVLLLLALLGFILPLPGVQALLCQFGTVQHVWVSDLPQWTPKNTSCDSGLGCQDTLMLI
 ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
 PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTTHCYDGLRLRGGGIFSNLRVQGCMPQPGCN
 LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSTNTEMCEVGQVCQETL
 LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
 SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGC
 VAQPSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESALTWCVGLALAPALWWGVVC
 PSC

FIGURE 251

GCGACGGGCAGGACGCCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCTCCTGCCTGCGCT
 CAGGATGAGGGGGAATCTGGCCCTGGTGGCGGTTCTAATCAGCCTGGCCCTCCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGGACGGCCTGGAAGAGTCG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTGCTCAT
 GGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCTTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCACAGTGTCTGCCAGGGCCGCGGGGCGACGCTGAGCATGCCAAGGACGAGGCTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGCCCCGTGTCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
 CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
 GAGAACATGTGAGCCTCAGGCTGGGGGTGCCCATTTGGGGGCCCCACATGTCCCTGCAGGGTT
 GGCAGGGACAGAGCCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG
 AAAGTGTTCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
 ATGTCATTATGTAATTATTACCCAGAATTGCTCTTCATAAAGCTTGTGCCTTTGTCCAAGC
 TATACAATAAAATCTTTAAGTAGTGAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA

MRGNLALVGLVISLAFSLSPSGHPQFAGDDACSVQILVPLGLKGDAGEKGKGPAGPRGPRVG
PTGEKGDMDGDKGQKGSVGRHGKIGPIGSKGEKDSGDIGPPGPNGEPGLPCECSQLRKAIGE
MDNQVSQLTSELKFIKNAVAGVRETESKIIYLLVKEEKRYADAQLSCQGRGGLTSMFKDEAAN
GLMAAYLAGAGLARVLFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVAS
GGWNVDVACHTMYFMCFDKENM

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
 CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCTAGCCAGTTCCCTTGATCCTGCCAGACCACC
 CAGCCCCGGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT
 CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
 TTCTTGGCGGGGGCCGAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
 AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
 GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
 GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCCTCGGCC
 CTTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
 TTTTAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCAGCTTTGGCATCCTCAAGT
 ATCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
 TTTCCCTGTCCCAATCCCCAGGTGCGCACGCTCCTGTTACCCCTTCTCTTCCCTGTTCTTGT
 AACATTCTTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAAACTGCA
 TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCCTGTAGTGT
 CCTACATTAATAATATAATGTCTCTCTATTCCTCAACAATAAAGGATTTTGCATATGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPKSRDMHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:**Signal peptide:**

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCTGCTGTGCC
 CGCGCTGTGCCCGCTGTCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCCGTGAGTC
 CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCCTGGGTGGTGTATCCCTTGGGGC
 TGCTGTTCCCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCAACGTCACTCTCTTAGAGGAG
 CTGCTCAGCAAATACCAGCACACGAGTCTCACTCCCGGGTCCGAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCGGGGGTGGGGC
 CTGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTTGTTTGTGTT
 TTGAGACAGGTTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG
 AAACCTTAGACTCCCGGGGTAAAGCATCTGCTTCAGCCTCCCAAGTAGCTGGAACCTACAG
 GCATGCACCATGGTGCCAGCTAGATTTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT
 TGCCAGGCTGGTCTTGAACCTCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCACCCCTGTCTGGCTCTGGCTCTGTTCTTAACATCTTGCCAAA
 ACAACACACGTGGGTTCCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCGAGTGGGGAGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTTCCACTTGGAGAGTCCTTCCTCGCGTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACCGGGAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCCCTCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCACAGTCTTCAGG
 TGGAACCTTCCTTCCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCAGG
 GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTCAGCTATGAATGGCTT
 TTTAAACAAACCCAGCTCCAGCCTGGGTAACATGGTAAAGCCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGCGCACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCCTCCAGCCTGGGTGACAGAGCAAGACCTGTCTCAAAA

FIGURE 256

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSAAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGLRVSSGR
GGSRLCSVLVFCFETGSHSATDAGVQWHNRHALKP

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GG
GTCTGGGCTGCCCCCTTGTCCTCCTCTGACCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC
TTCTTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCCTG
TGTCTTCTTGGCCCGGGCTTTTGGGCCGGGATGCAGGAGGCAGGCCCCGACCCCTGTCTTT
CAGCAGGCCCCACCCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

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FIGURE 258

MGSGLPVLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSTGTS
VTLHHARSQHHVVCNT

$\begin{pmatrix} p_1 \\ p_2 \\ p_3 \\ p_4 \\ p_5 \\ p_6 \\ p_7 \\ p_8 \\ p_9 \\ p_{10} \\ p_{11} \\ p_{12} \\ p_{13} \\ p_{14} \\ p_{15} \\ p_{16} \\ p_{17} \\ p_{18} \\ p_{19} \\ p_{20} \\ p_{21} \\ p_{22} \\ p_{23} \\ p_{24} \\ p_{25} \\ p_{26} \\ p_{27} \\ p_{28} \\ p_{29} \\ p_{30} \\ p_{31} \\ p_{32} \\ p_{33} \\ p_{34} \\ p_{35} \\ p_{36} \\ p_{37} \\ p_{38} \\ p_{39} \\ p_{40} \\ p_{41} \\ p_{42} \\ p_{43} \\ p_{44} \\ p_{45} \\ p_{46} \\ p_{47} \\ p_{48} \\ p_{49} \\ p_{50} \\ p_{51} \\ p_{52} \\ p_{53} \\ p_{54} \\ p_{55} \\ p_{56} \\ p_{57} \\ p_{58} \\ p_{59} \\ p_{60} \\ p_{61} \\ p_{62} \\ p_{63} \\ p_{64} \\ p_{65} \\ p_{66} \\ p_{67} \\ p_{68} \\ p_{69} \\ p_{70} \\ p_{71} \\ p_{72} \\ p_{73} \\ p_{74} \\ p_{75} \\ p_{76} \\ p_{77} \\ p_{78} \\ p_{79} \\ p_{80} \\ p_{81} \\ p_{82} \\ p_{83} \\ p_{84} \\ p_{85} \\ p_{86} \\ p_{87} \\ p_{88} \\ p_{89} \\ p_{90} \\ p_{91} \\ p_{92} \\ p_{93} \\ p_{94} \\ p_{95} \\ p_{96} \\ p_{97} \\ p_{98} \\ p_{99} \\ p_{100} \end{pmatrix}$

FIGURE 259

AATTGTATCTGTGTAATGTTAAAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAGAAGCTCTTTAAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGTTCCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTCGAGAAGCTTCATTAGTGTGAAATGAATGCTTAGTGGATCTG
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCCTCCC
CTCCGATTGTTCTAAA**TAA**TTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCATGGAAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAAATAGAAACCTGTGTTTATTTCTCAGGTATTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTATAAAATTATATATTTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAACCAATTATGTTTGTAAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

FIGURE 260

SDCSK

Signal peptide:

amino acids 1-29

[illegible]

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACGGAGCCCTTGAGACATCCTT
GAGAGAGGCCACGACATAGAGCATGCCCCTGCTTGGTGTTTTGCGAGGATGATGGTGGCCCTT
CGAGGAGCTTCTGCATTGCTGGTTGCTGTTCTTGCAGGCTTTTCTGCCCCGCCGACGTATC
CGAGGACCGGACGATGTGTGCATTACATCTACCAGCGCTTTCGAGTCTTGAGACAGGGCTGG
CAAAGATGTACCAAGCAAGCAGGGGACATACATTCAAGATTCACAAAGTTCTCAA AAAATATA
TCTGTCTGCTGGGAAGATGTCAGACCTACACAAGTAGTACAAGAGTGCAGTGGGTAACTT
GGCATCTGAGAGTTGAACGTGGCCCAAGCGGAGATTGACTACATACATACCTTCGAGAGGCTG
ACAGTGCATCGTATCAGAGGACAAGACATGGCAGAAATGTTGCTCCAAGAAGCTGAAGA
GAGAAAAGATCGCGGACTCTGCTGAATCAAGCTGTGACACAATGCTGTGGGCATAAAGTC
TTTGAATAAGTGAAGAAGATGTAGGACACATGGCTCTTGGATGAAGATGCTGTCTATA
ACTCTCCAAAGGTGTACTATTATTAATTTGGATTCCAGAAACCAACACTGTTTGGGAATTGTCAAAC
ATACGGCCATTCATGGAGATAAACACAGCCGACTCCCGGAAGCAAACTCTAACACTTTC
CTGGCAGGGAACAGGCCAAGTGTCAACAAGGTTTCTATTTTTCATACCAACCAACTT
CTAATGAGATAATCAAATATAACTGCAAGAGGACTGTGGAAGATGCAATGCTGCTCCCA
GAGGGGTAGGCCGAGCATTTGGTTTACCAGCATCTCCCCTCAACTTACATTGACCTGGCTGT
GGATGAGCATGGGCTCTGGGCCCTCCACTCTGGGCCAGGCCATAGCCATTTTGGTTCTCA
CAAGAGTTAGGCGCGGCACACTGGGATGGAGCATTCATGGGATACCCATTGCAAGAGCCAC
GAGTCTGAAGCCTTATTCTCTTGTGTGGGTTCTCTATGTGTGCTACAGTATGGGGGCCA
GGGCGCTCATCGCATCACTGCATCTATGATCCACTGGGCATATCAGTAGGAGGAGATTCG
CCAACCTGTTCTTCCCAAGAGCAAGAAAGTCACTCATGATTCATTACACCCCAAGAGAT
AAGCAGCTCTATGCTGGAAATGAAGGAAACAGCATACTTTACAACCTTCAGACAAGAGAAA
GCTGCTCTGAACTTAATACAGCTGTGAGAAAGAGCATCTGGCTTTGGCAGCTGTTCT
TACAGGACAGTAGGGCTATAGCCCTTACAATATAGATTATCTCTAATCACACAGGAAAG
AGTGTGTAAGAGTGAATAACGATAGCTCTCTTCCCAAGTGTACTGCTTAGTATCTCT
CAAGAGCTTAGATGAGGACATATCATCAGGAAAGTTCAACAATGTCCATTCTTCCCAAA
CTCTCTGGCTCTCAAGGATAGCCACTTCTGATACAGCTCTACTCAGCGCTTTGTTTATA
GCTCCCAGCATTTACTGTAACTTGCCACTTCTCCCTCCCAACATTAGAGTTGATGCGCAGC
CACTAATATTCACCACTGGCTTTTCTCTCCCTGGCCTTGTGTAAGCTCTTCCCTTTCT
CAAAGTGCTATTGATATCTCCCATTTTCTAGTCCCACTAAAATACTATTATATTTCTTT
CTTTTCTTTTCTTTTGTGAGACAAGGCTCTCAATATGTTGCCAGGCTGTCTCAACTCC
AGAGCTCAAGAGATCTCTCGCTCAGCTCTCAATAGTAGCTGGGATTACAGGCATGTGCCAC
CACACTGGCTTAAATACTATTCTTATGAGGTTTAACTCTATTCTTCCCTAGGCCGTCT
CTTCACTAAGCTTGGTAGATGTAATTAAGAGTGAATAATTAACATTTGAATATGCTTT
CCAGTTGTGGAGGTTTGACATCATTTGAATTTCTGTTTACCTTTGTGTAACATGCACAG
TCTTTACAGCTGTCACTTAGAGTTTAGTGAGTAAACAATAACAAGTGAAGATACAGC
TAGAAAATACTACAATCCCATAGTTTTCATTGCCCAAGGAAGCATCAATACGTATGTT
TGTCTACCTACTCTTATAGTCAATGCTTCTGTTTCAAGCTAAAAATAAGTCTGTGCT
TTTAGCCAGTTTCTATGCTGCACAGACCTTTCATAGGCCTTCAAATGATAATTCTCC
AGAAAACCAAGTCTAAGGTTGAGGACCCCACTATGCCCTCTGTCTGTCTGCTCTGT
TCTCTCTTCTGCTTTAAATTCAAATAAGGTGACATGACGCAAAAAA

MMVALRGASALLVFLAAFLPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCTYTSEYKSAVGNLALVERAQRIDYIQYLREADECIVSEDKTAEMLL
QEAEEEKKIRTLLNASCDNMLGIKSLKIVKMMDTHGSWMKDAVNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAAPRKQILTLWSQGTGQVIYKGLFFHNQATSNEIKYNLQKRTVED
RMLLPGGVGRALVYQHSPTSYIDLAVDEHGLWAIHSGPGTHSHLVLTKEIPGTLGVEHSWDT
PCRSQDAEASFLLCGVLVYVYSTGGQGPHRITCIYDPLGTISEEDLPNLFPPKRP RSHSMIH
YNPRDKOLYAWNEGNIQIYKLTQKRKLPLK

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPDPKSSGSKKQK
QYQRIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSKDFLQ
REHRSMRANVELDHATLVRFSPDCRAFIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNTHAAVSPCGRFVASC
FTPDKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHILKRASNESTRQLQQQLTQ
AQETLKS LGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTTTTGCTTACCCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC
 TCCTAGTAACGTGTCTGACTGTGCTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT
 GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCA
 AGCACCCACCTGTCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATTTTTTAGCGCTTGCTGCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTTTATTTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCAGTCCCTACACTGACTACCTGATCTCTCTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCCCCTCCCCCTCCCGAGGTGACCTGCTCTCTTCTGGGCCCTG
 CCCCTCTCCCCACATGATCCTTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCCAGGTCCTGGCCTGACCTCAGGCCCTTACGTTAGGTCGTGTGAGG
 ACCAATTTGTGGGTAGTTTATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCCAGAC
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCTCTTACCACACTTTACCAGT
 TAACCACTGAAGCCCCCAATTCCCACAGCTTTCCATTAAATGCAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTTCTTAAACAACCTCTTTCCA
 AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTAGACACAGGGAGG
 CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHP
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

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FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTAAAGGCCGGCAGAAGGGAGGCACTTGAGAAATGTCCTTTC
 CTCCAGGACCCAAGTTTCTTACCATTGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGGTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG
 CCTTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA
 GCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAGGAGCACATCAGGACTGAAGTGAAGGATTTCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGCGGAAGAT
 GATGTTTATGGATTTATCCGTCTGGGAGTGTGGTACAACCTCTTCCGAGCCTGGAACGGAG
 GCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCTGGTGGGATCA
 GGAAGCAGGGCATCTTCTTGTAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAAATGAT
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTTATGGGATGTATT
 GTTTCCTCTCGTGTCCCTAAGGAGTGAGAAACCCATTATACTCTACTCTCAGTATGGATTA
 TTAATGTATTTTAATATCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGA
 CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACTTGAGGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACTTGAACTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
 CACCAGTGTATTCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLLANTDVFLSKPQKALEYLEDIDLKTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMQLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIPLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLEGEGLGGVVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCG
GGCCAGGTGCCCCGTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCCTCGGCGCTGCCAACC CGCCACCCAGCCCCATGGCGAACCCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCGCTGCCGTTCCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATCTAGGTCCCCTCTCCTGCATCTGTCTCC
CTTCATGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

MANPGLGLLLALGLPFLRLRWGRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIV
VFSLLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

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FIGURE 271

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTT
TTGGGATTTTAAATTTTCAAACACAGCAGAAATGACATTTTTCTGTCACATATTATTATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTAAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAA

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

[illegible]

[illegible]

FIGURE 274

MGLFRGRFVFLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTY
 LFEATEKRFFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
 CSAGISGRNRVYKCGGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMSIDSVVE
 FCNEKTHNQEAPSLQNIKNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLLKISQRIVCLV
 LDKSGSMGGKDRNLNRMNQAAKHFLQLTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTGDGNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKIITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPSPISLWDPSTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNKDVNSFPSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNQGVYSRYFTAYTENGYSYSLKVRAGH
 GANTARLKLRLPPLNRAAYIPGWVNVGEIEANPPRPEIDEDTQTTEDEFSRTASGGAFFVSQV
 PSLPLPDQYPPSQITDLDTVHEDKIIILTWTAPGDNFDVGKVQRYIIRISASILDRLDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNNIAQVTLFIP
 QANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.
 amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
 628-632, 811-815, 832-836, 837-841, 852-856, 896-900

[illegible]

FIGURE 276

MMMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALFRANSPTGKEGYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIES
ALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKEFKRLILFRPFSP
MKVKNEKLNMAANTLINIVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYPVLF SQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVRTPVRLFHLWHEKRCMDELTPEQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQTSSKKT

FIGURE 277

GAAAGAAATGTTGTGGCTGCTCTTTTTCTGGTGACTGCCATTTCATGCTGAACTCTGTCAACC
 AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCTCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGCTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACT
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAACATGATCACAATTGAAAATGGCATCCCTCTGATCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCTTCATGAAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTCTGCTTCTCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA
 CCAAGAGCAGATCATATATTTGTTTCACCATTCCTCTTTTGAATAAATTTTGAATGTGCT
 TGAAGTGAAGAAAGCAATCAATTATACCCACCAACACCCTGAAATCATAAAGTATTCACGAC
 TCAAAATATTCTAAAAATATTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
 TAGTTATTGATTTAAGCATTTTGTAGAAATAAGATCAGGCATATGTATATATTTTACACTTC
 AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAAAATGGATCCTTTTGGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
 TGAGAAATTAATTATTGTAAATGGATGGATAAAATGGAATTACTCATATACAGGGTGGAAAT
 TTATCCTGTTATCACCAACAGTTGATTATATATTTTCTGAATATCAGCCCTTAATAGGAC
 AATTCTATTTGTTGACCATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTTAAAAA

FIGURE 278

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQRVSFVFTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTL
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGILMMP

FIGURE 279

AACTCAAACCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATGT**
 ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATACAGCTCACAGCTCTTTGG
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAATGCACTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
 ATTTTCGTCTCTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA
 TGCTCCATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTCTGAGATCCACTTCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
 GTTTATTTAGAAGACACAGAC**TAA**CAATTTTAGATGAAGCTGAGATGATTCCAGAACA
 GAACCCTAGTATTTCTGAAGTTAATGGAACTTTTCTTGGCTTTTCCAGTTGTGACCCGT
 TTTCCAACCAAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTCAGA
 GTGTAAATTTTTCAAGTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTTGCCCTTAA
 GACACTACTTACAGTGTATGACTTGTATACACATATATTGGTATCAAGGGGATAAAAGCC
 AATTGTCTGTACATTTCCCTTTCACGTATTTCTTTAGCAGCACTTCTGCTACTAAAGTTA
 ATGTGTTTACTCTCTTCCCTCCACATTCTCAATTAAGGAGGCTAAGCCTCCTCGGTG
 TTTCTGATTAACAGTAAATCCTAAATTCAAACTGTTAAATGACATTTTTATTTTTATGTCTC
 TCCTTAACATAGAGACACATCTGTTTTACTGAATTTCTTTCAATATTCCAGGTGATAGATT
 TTTGTCG

FIGURE 280

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQFVFYYHIDPFQPMSEGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVDGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVVVVLFQHYRKKRWAER
AHKVVEIKSKEEERLNQEKKVSVYLEDTD

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FIGURE 281

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCAACACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCTCTGCTGATGATGAAGCCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCTT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATATTCATGCTTCCTGTGATTC
ATCCAACACTTACCTTGCTTACGATATCCCCCTTATCTCTAATCAGTTATTTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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FIGURE 282

MKFLAVLVLLGVSIFLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTAT
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FIGURE 283

GGACTCTGAAGGTCCAAGCAGCTGCTGAGGCCCAAGGAAGTGGTTCCAACCTTGGACCC
CTAGGGGTCTGGATTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGA**AATGC**
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
GTGTCCTGGGTCAGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG
GCAAACTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAG**TAA**AACCACAGGCTGG
ATTTGCCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
CCCCAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTA¹AAACTGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCAC**TGG**TAGTCCCAGTTACTCGGGAGGCTGAG
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

FIGURE 285

GTCATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCTGCTCTTCCATGG
GACCCTGCACTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC
CGGGGCCGGGATGCAGCCAGGAACTTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCAGCCTGAATCTGCCTGGATGGAAGTGA
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
GCAGGCGGGGACAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
CCCTTTTCATGCCTACACACCCCTCATTAAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

MPVPALCLLWALAMVTRPASAAPMGGPQLAQHEELTLFHGTLQLGQALNGVYRTTEGR¹LT²K³
ARNSLGLYGR⁴TIELL⁵GQEVSRGRDAAQELRASLETQMEEDILQLQAEATAEVLGEVAQAQ⁶K⁷
VLRDSVQRLEVLQ⁸LRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAAQ⁹HR¹⁰L¹¹R¹²
IOERLHTAALPA

FIGURE 287

GGCAAC**ATG**GCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAAATTTGCAT
 CCTGGTGATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAGGCCAGGA
 AGCAGAGCAAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTTGAAAAGCTC
 TGGACAGAAGTCAATGCCCTGAAGGAAATTCAGGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTCACAAAGAAATGTACCTTGCTTCAGAAGGTTTGAAGCATTTCATGAGGCCAATG
 AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAATCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTGTGACGTCAACGGAATCGCTATCTCCTTCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAACCTGTGTCTGTCTCCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCCTGTGCGAGCAGCAAGAGATACATATGCGAGTTCACCATCCC
 TAAAT**TAG**CTCTTTCTCCAATGTGTCTCCAAGCAAGATTCATCATAACTTATAGGTTTATGA
 TCTCTAAGATCAAGTAAAAATCATAATTTTACTTATTAATAAATTGCAACACAGATCAAT
 GTCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
 AAACAGACTAAAATCTTCTCTAGTCTTTCTCACTTGTACAAAACCCAGTTTGTTTTCAAA
 AAATCACAGTAGCAATGCAACTCATCACTTAGAAAAGCAAGCTTAGGCTACCTGAAGATT
 TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATCCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAAACCTTTTCAGCCTGTTGCTCATCTGTCCCATGCTGGCAATAATACC
 TTGTGAGCCCATACCCCTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCC
 TACCCCTTTTTTGGAGGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTGTAT
 CAATTTTCATTCCCACCATTCGATTACAACCTCTAACTTAAATGGGTAACCCCTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAAATAGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTTTACATTT
 TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATCTT
 TGGAGCTGAAAACCTGAATTTAAAGAATGCTATCTGGAAAATTGATACGCTCTGTGCAATT
 TTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAATAACTTCATTGCT
 TAATATCAAATTACAAAGTTTAGACTTGGAGGGAAATGGGCTTTTTAGAAGCAAACAATTTT
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTGTGAACAATAT
 CCCACTTTGCAAACTTTAACTACACATGCTTGGAAATTAAGTTTATAGCTGTTTTTCATTGCTCA
 ATAATAAGCCTGAATTCGTATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCCGGGCAGCCGAGGTTCCCCGCGGCGC
CCCGAGCCCCCGCGCCATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCA
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTCGCTGCGCTG
GAGTCGGCGGCGAGGCCGGGGCCGGGACCTTGGCCAACCCTCGGCACCCCTCAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGGCTGAAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCCTCCCCCGGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 290

MKLAALLGLCVALSCSSAAAFVLGSAKPVAQPVAALESAAEAGAGTLANPLGTINPLKLLLS
SLGIPVNHIEGSQKCVaelGPQAVGAVKALKALLGALTVFG

FIGURE 291

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACT
 CCTTGGCCTCCGACGGCATCAC**ATGA**AGGTGGTGCCAAGTCTCCTGCTCTCCGTCTCTCCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCTCCTCAGTCGCCAGAGACCCAGCCCC
 TCAGAAACCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTTCGGATTGAGCCTGCTGCCAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTGGCATGTCTTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCACCAAG
 CCCGGCTCCTGCCCTTCCCTCTTTAAGGGACTCAGAGAGACCTCTCCCGCAACCTGGAAC
 TGGCCTCTCACAGGGAGTTTGGCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGCCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGGAAAATTCCCAAAC
 GTTTGATGAGATTAATCCTGAAACCAATTAATCTTGTGGATTACATCTTGTTCAAAGGGA
 AATGGTTGACCCCATTTGACCTGTCTTACCAGAGTGCAGACTTTCACCTGGACAAAGTAC
 AAGACCATTAAAGTGCCCATGATGTACGGTGCAGGCAAGTTTGGCTCCACCTTTGACAAGAA
 TTTTCTGTTGTATGTCCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCA
 TGGAGAAAATGGGTGACCACTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAACATGAAAACAGAAACATGGAAGTTTCTTCCGAAGTTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCTTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAAATTAC
 TGCTTATTCATGCCTCCTGTATCAAAGTGGACCGGCCATTTCAATTCATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTAT**TA**ATTCAAG
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCTTTTGTCTTAACTAGTTTAGGGTGTCTC
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTGTCTGAACCTTATATATATTTTTTCTTACACATACATACCTATGAT
 AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAACAATAATAACAACATTAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGCGAGGAGCATAGACAGTGTGGAGACATTTGGGCAAGGGGAGAAATCA
 CATCTGGGTGGGACAGAGCAGGACGATGCAAGATTCATCCCATCTACTCAGAATGGCATGC
 TGCTTTAAGACTTTTAGATTGTTATTCTGGAATTTTCATTTAATGTTTGGACCATGGT
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAAACCATGGATGAAGGAGGACTACTACAAAA
 GCATTAAATTGATACATATTTTTTAAAAAAAAAAAAAAAAAAAA

FIGURE 292

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F
L G R V V N P T L L

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGAC**ATG**AG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGTCTCC
TGTCAGAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGTCTGAGTCCC
GAGCCCAGCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGAGGAAGACCAAGACCACA
TCTACCACCCCAG**TAG**GGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCCAAGGCCAGG
CTGTTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
AAAAAAAAAAAAAAAA

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
 TACCCAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGC
 TGTTTCTCATAGCACCACAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
 TGGACCTGTTCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
 TAGTGCAATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT
 GTGACATGACCTCTGGGGTGGCGGCTGGACCTGGTGGCCAGCGTGCATGAGAATGACATG
 CGTGGGAAGTGCACGGTGGCGGATCGCTGGTCCAGTCAAGGGCAGCAAAGCAGACTACCC
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
 ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
 CCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
 TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT
 ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCGTGATCCCTGTGGTCTATGATTTTGGC
 GAGGCCCAGAAAACAGCATCTTATTACTCACCCTATGGCCAGCGGGAATCACTGCGGGATT
 TGTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCCTTGTGTGCTGGAATGAGGG
 TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACCTTCCAGAGGCCAGT
 CCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACATGTTGGTTA
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTGTG
 GGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACTTACCCA
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDWRSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYYSYPYQGREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGGYFPEASPQCQDGSFGFDWSGYGTHVGYSSSREITEAAVLL
FYR

FIGURE 297

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGATCCTGCCCTCGGAACAATGGGA CT CGGCGCGCAGGTGCTTGGGCCG
 CGTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGCCGCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAACATAGAGAATTCTGGGCTTCACACAAC TCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAAACAACAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAAC TATGCAT
 TCTGAAGCAAAGAAAGGATCAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC
 GGTATCGAACCATAGATGAACATGATGCCATCATTTTAAGGAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCCTATCAATTAAATTTGGTTTATTAATAGTTTAAACAATATTCT
 CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAATATGTA
 AAGATTCTTCAAGGTAACAAGGTTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAACAAGTCTATCTTTTTTTTTGGCT
 GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAGACGTCATCACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT
 AGCTCACATAAAGAAC TTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAAC TAGATCTGAAGCATAA TTTAAGAAAAACATCAACATTTTTTG
 TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

FIGURE 298

MGLGARGAWAALLLGTLLQVLALLGAAHESAAMAASANIENSGLPNSSANSTETLQHVPSDH
 TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
 TSQISTSTMFTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG
 CKMYYSRRGIRYRTIDEHDAII

$\begin{pmatrix} p_{11}^{(1)} \\ p_{12}^{(1)} \\ p_{13}^{(1)} \\ p_{14}^{(1)} \\ p_{15}^{(1)} \\ p_{16}^{(1)} \\ p_{17}^{(1)} \\ p_{18}^{(1)} \\ p_{19}^{(1)} \\ p_{20}^{(1)} \\ p_{21}^{(1)} \\ p_{22}^{(1)} \\ p_{23}^{(1)} \\ p_{24}^{(1)} \\ p_{25}^{(1)} \\ p_{26}^{(1)} \\ p_{27}^{(1)} \\ p_{28}^{(1)} \\ p_{29}^{(1)} \\ p_{30}^{(1)} \\ p_{31}^{(1)} \\ p_{32}^{(1)} \\ p_{33}^{(1)} \\ p_{34}^{(1)} \\ p_{35}^{(1)} \\ p_{36}^{(1)} \\ p_{37}^{(1)} \\ p_{38}^{(1)} \\ p_{39}^{(1)} \\ p_{40}^{(1)} \\ p_{41}^{(1)} \\ p_{42}^{(1)} \\ p_{43}^{(1)} \\ p_{44}^{(1)} \\ p_{45}^{(1)} \\ p_{46}^{(1)} \\ p_{47}^{(1)} \\ p_{48}^{(1)} \\ p_{49}^{(1)} \\ p_{50}^{(1)} \\ p_{51}^{(1)} \\ p_{52}^{(1)} \\ p_{53}^{(1)} \\ p_{54}^{(1)} \\ p_{55}^{(1)} \\ p_{56}^{(1)} \\ p_{57}^{(1)} \\ p_{58}^{(1)} \\ p_{59}^{(1)} \\ p_{60}^{(1)} \\ p_{61}^{(1)} \\ p_{62}^{(1)} \\ p_{63}^{(1)} \\ p_{64}^{(1)} \\ p_{65}^{(1)} \\ p_{66}^{(1)} \\ p_{67}^{(1)} \\ p_{68}^{(1)} \\ p_{69}^{(1)} \\ p_{70}^{(1)} \\ p_{71}^{(1)} \\ p_{72}^{(1)} \\ p_{73}^{(1)} \\ p_{74}^{(1)} \\ p_{75}^{(1)} \\ p_{76}^{(1)} \\ p_{77}^{(1)} \\ p_{78}^{(1)} \\ p_{79}^{(1)} \\ p_{80}^{(1)} \\ p_{81}^{(1)} \\ p_{82}^{(1)} \\ p_{83}^{(1)} \\ p_{84}^{(1)} \\ p_{85}^{(1)} \\ p_{86}^{(1)} \\ p_{87}^{(1)} \\ p_{88}^{(1)} \\ p_{89}^{(1)} \\ p_{90}^{(1)} \\ p_{91}^{(1)} \\ p_{92}^{(1)} \\ p_{93}^{(1)} \\ p_{94}^{(1)} \\ p_{95}^{(1)} \\ p_{96}^{(1)} \\ p_{97}^{(1)} \\ p_{98}^{(1)} \\ p_{99}^{(1)} \end{pmatrix}$

FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCGATGCGCACCCCTGTGGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTGCTGCCTGGCGCTTCCGTGCTGCTGCTGGC
 GCAGCTGTGAGACGCCGCCAAGAAATTCGAGGATGTCAGATGTAATGTATCTGCCCTCCCT
 ATAAAGAAATTCGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
 CATGTTGTGGAGCCCATGCCTGTGCGGGGCCCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCATACTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
 TGCAAATGCACACGATGTGCTAGCCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG
 CATGTTGTCTCAGCTTAATGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTACCAACT
 GTTGCTGGAAGATTCAAACTGGAAGCAAAAACCTGCTTGATTTTTTTTCTTGTTAACGTA
 ATAATAGAGACATTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTG
 TGACTTTTACTAATAAAAAATAAATCTGCCTGTAAATATCTTGAAGTCCTTTACCTGGAACA
 AGCACTCTCTTTTTACCAACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG
 TTGTTGTTGTTTTTTGTTTGTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTT
 AACAACTTTTTCAAGTCACTTTACTAAACAACTTTTGTAATATAGACCTTACCTTCTATTT
 TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG
 ACTTTTGCACTGACTGTATTATCTGGGTATCTGCTGTGCTGCACTTCATGGTAAACGGGAT
 CTAAAAATGCCTGGTGGCTTTTCAAAAAAGCAGATTTTCTTCATGACTGTGATGTCTGATG
 CAATGCATCCTAGAACAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG
 GTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
 TGCAATAAAGAAATTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACATTTG
 TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAAC
 AGGGCTGGGGTTGTGGTGCCCTCTTCTGAAAGGTCTAACCATTTATGGATAACTGGCTTTTT
 TCTTCCTATGTCTCTTTGGAATGTAACAATAAAAAATAATTTTGAAACATCAA

FIGURE 300

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FIGURE 301

GCACCTGCGACCACCGTGAGCAGTC**ATG**GCGTACTCCACAGTGCGAGAGAGTCGCTCTGGCTT
CTGGGCTTGCTCTGGCTCTGTCGCTGCTGCTGCCAAGGCCTTCCTGTCCCGCGGAAGCGG
CAGGAGCCGCCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAAT**TGA**AAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTTCAGTTTCACATAAGAATG
TTTACTCAATGTTTAAGTGTTTTGCCCCAAAATTCACAACATAACAAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

FIGURE 302

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGREFPPMMHHHQAPSDGQT
PGARFQQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIPIYGFGIPLYILYILFKVSRIILI
ILHQ

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCCTCCCCCTGGGTGCTCTTCATCTT
 GGATTGAAAGTTGAGAGCAGC**ATG**TTTTGCCCACTGAAACTCATCTGCTGCCAGTGTTAC
 TGGATTATTCCTTGGGCCCTGAATGACTTGAAATGTTCCCCGCTGAGCTAACAGTCCATGTG
 GGTGATTTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT
 AGACTGGAGCTCTGTACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
 ATCTCAGTGTGCCTATTGGGCGCTTCAGAACCCGCTACACTTGATGGGGGACATCTTATGC
 AATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
 AATCCGCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGGTACTGCATGTGCTTCCAG
 AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTCAGATGGGATGTGTTTTCCAG
 AGCACAGAAGTGAAACAGTGAACCAAGGTAGATGGAATATTTTCAGGACGGCGCGCAAAGGA
 GGAGATTGTATTTCTGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
 GCCACTTCCAGAATCGTGTGAACCTGGTGGGGACATTTTCCGCAATGACGGTTCATCATG
 CTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACTCT
 GGTGTTCAAGAAAACCATTTGTGCTGCATGTGAGCCCGAAGAGCCTCGAACACTGGTGACCC
 CGGCAGCCCTGAGGCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTTGTGGGAATTGTC
 TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
 GAGTTCAGTGAATTCTACAGCTCTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
 AAAAAACCCTGCCATTTTGAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA
 CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAATAATCAGAGGCCACCTACATGACCATGCA
 CCCAGTTTGGCCTTCTCTGAGGTGAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG
 GAATGCCAAAAACACAGCAAGCCTTT**TGA**GAGAATGGAGAGTCCCTTCATCTCAGCAGCGG
 TGGAGACTCTCTCTGTGTGTGCTCGGGCCACTCTACCAGTGATTTCAGACTCCCCTCTC
 CCAGCTGTCTCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
 CTCTGGAGTGGGACACTGGCCCTGGGAACCAAGGCTGAGCTGAGTGGCCTCAAACCCCCGTT
 GGATCAGACCTCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
 AAAACCAACCCAAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSGLNDLNVSPPELTVHVGD¹SALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYY²SNLSVPIGRFQNRVHLMGDILCNDG³SLLLQDVQ⁴EADQGT⁵YICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGG⁶LQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKL⁷RMSVEYSQSWGHFQNRVNLVGDI⁸FRNDGSIMLQGVRES⁹DGGNYTCSIH¹⁰LGNLVFKKTIV
LHVSP¹¹EEPRTLVT¹²PAALRPLVLGGNQLV¹³IIVGIVCATILL¹⁴LPVLILIVKKTCGNKSSVNSTV
LVKNTKKTNP¹⁵EIKEKPCHFERCEGEKHIYSP¹⁶IIVREVIEEEEPSEKSEATYMTMHPVWPSLR
SDR¹⁷NNSLEKKSGGMPKTQQA¹⁸F

FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG
 GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATGTAGAGTTGG
 AAACACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATG**CA
 GGATGAAGATGGATACATCACCTTAAATATTAAAACTCGGAAACCAGCTCTCGTCTCCGTTG
 GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
 ATGGTTGTTCGGGCTGGTGGCTCTGGGGATTGGTCTGTGCATGCAGCGCAATTACCTACAAGA
 TGAGAATGAAAATCGCACAGGAACCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
 TAAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCCTGTGACACAAAC
 TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTAACATGGGAAGAGAG
 TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
 AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
 GAGGTC TGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGGAAGA
 TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCTACCTTCTGTG
 AGAACAACACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATGTACAATAAAAGATATGT
 ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

MQDEGDYITLNIKTRKPALVSVGPASSSWWRVMAILLILLICVGMVVLVALGIWSVMQRNYL
QDENENRTGTLLQQLAKRFQYVVKQSELKGTFKGHKSCPCDNTWRYYGDSYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVLSRQKSNEVWKWEDGSVISENMFEFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

FIGURE 307

CCCACGCGTCCGCGCAGTTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGCGATCCCGG
 CCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGGGAGCCGGACCGC
 CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGGGAGAA
 GCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
 CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCGAGAAAAGAAGCGGTGGTGGTGGG
 CGTCGTGGCC**ATG**CGCGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG
 AGCGCGAGAAATCCAACGCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
 GACAAAAACAAGTTAAATGTCTTTTCCCGGTCAAACCTCTCGGCTCCAAGAAGAGGCGCAG
 AAGAAGACCAGAGCCTCAGCTTAAGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
 ACTTGCAGCTGCAGGCGGATGGAACCATTTGATGGCACCAAAGATGAGGACAGCACTTACACT
 CTGTTTAACTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTCAAACCAAGCT
 GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTCACACCTGAGTGCA
 AATTCAAAGAATCAGTGTTTGAATAATTATTATGTGACATATTCATCAATGATATACCGTCAG
 CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
 CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
 ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
 AAGAGCGAAAGTGTCTCTGGCGTGTGAACGGAGGCAAATCCATGAGCCCAATGAATCAAC
GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAAACGAACCTTACCTCCAGTGCTGTTGAAT
 TCTTCTAGCAGTCCCTCACCCAAAAGTTCAAATTTGTCAAGTACATTTACCAACAAACAGG
 CAGAGTTCACATATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGTSCDKNKLNVFSRVKLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSELFTPECKFKESVFENIYYVTYSSMIYRQQSGRGWYLGlnKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKRSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATCTGAGACATATTTTGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCT
 CCATTTAGAGTGTAGCAAAGGAAAAACCAAGGTGGGGTTCCTTCTGACATTGGCAGTG
 CCCCAGTAGGGGTGGGATGAGCGAATATTCCAAAGCTAAAGTCCACACCCTGTAGATTAC
 AAGAGTGGATTGGCAGGAGTGTGCCCAAATACAGTGGAAGGTGCCTGAAGATATTTAA
 ACCACGTCTTGAAATTTAGTGGGTCTTGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGGAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTGGTAACCTGGCTGCT
 GTGGAGGGGGGTACGTGAGGGGGGGTCTGGGGCTTATCTCAGGTCCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG
 CGCGCTCCGGCGCCTGCCGGTTTGGGGGTGTCTCCTCCGGGGCGCTATGCGCGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGGCAGCCCGGGGGCAGCCGGCCGGTGTCCG
 CGCAGCGGCGCGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGGGCGCCCGCGCGGCGGACCGCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAACCTGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGCTCCTTCACCACTTCAACCTGATCCCT
 GTGGGCCTCCGTGTGGTCAACATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTCCGCCGATTTACAGCTGAGTGTGCTCTTAAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCAAGAAGGAAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCCCTGAATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIRQKREVREPGGSRPVS AQRRVCPRGTSKLCQKQLLILLSKVRLCGGRPARPDR
 GPEPQLKGIVTKLFCRQGFYLQANPDGSIQGTPEDTSSFTHFNLI PVGLRVVTIQSAKLGHY
 MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRSSGRAWYLG LDKEGQVMKGNR
 VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACC GGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGC GCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACTCT
TCAACCTCATACCAGTGGGACTACGTGTGTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGACCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAGAAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAAACAGTCAACAAGAGTAAGACAACA**TAG**

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDSPASRRRSSPSKNGRLCNGNLVDIFS KVRIFGLKKRRLR
RQDPQLKGIVTRLYCRQGYLQMHPDGALDGT KDDSTNSTLFNLI PVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELF TPECKFKESVFENYYVIYSSMLYRQ QESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGTGCCTTGCAAAAAAT
 GAAGGATGCAGGACGCAGCTTCTCCTGGAACCGAACGCAATGGATAAAGTATTGTGCAAGAGAGAGGAAGA
 ACCGAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGAGCATTCAAGAATG
 AATAAACCCAGAGTTAGACCCCGCGGGGTGGTGTGTTCTGACATAAATAAATATCTTAAAGCAGCTGTCCCC
 CTCCCCACCCCCAAAAAAGGATGATGCAAATGAAGAACCGAGGATTACAAAAGAAAAAGTATGTTCAATTT
 TTCTCTATAAAGGAGAAAGTGAGCCGAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAA
 AGAAGTGGTGTGGTGGTGTTCCTTTCTTTTTGAATTTCCACAAAGAGGAGAGAAATTAATAATACATCTGC
 AAAGAAATTTAGAGAGAAAAAGTTGACCCGCGCAGATTGAGGCATTGATTGGGGAGAGAAACAGCAGAGCA
 CAGTTGGATTTTGTGCCTATGTTGACTAAAATTGACGGATAATGACAGTTGGATTTTTCTTCATCAACCTCCTTT
 TTTTTAAATTTTTATTCCCTTTTGGTATCAAGATCATGCGTTTTCTCTGTTCTTAACCACTGGATTTCCATCT
 GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTGAATTCGAAGGACCAACACAGATAAATATG**AAAG**
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAACAGGGCCCTATTGACCCCT
 GCTTGTGGTGTCTGCTGGCTCTTCAACTTCTGTGGTGGCTGTTGTTGCGGGCTCAGACCTGCCCTCTGTGT
 GCTCCTGCAGCAACCACTGTCAGCAAGGTGATTTGTGTTGCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCC
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCAGTCCAGATCATCAAGTGAACAGCTTCAAGCACTTGAG
 GCACTTGAAAACTCTACAGTTGAGTAGGAACCATATCAGAACCATGAAATTTGGGGCTTTCAATGGTCTGGCGA
 ACCTCAACACTCTGGAACCTCTTTGACAATCGTCTTACTACCATCCGAATGGAGCTTTTGTATACTTGCTAAA
 CTGAAGGAGCTCTGGTTGCGAAACAACCCCATGAAAGCATCCCTCTTATGCTTTTAACAGAAATTCCTCTTT
 GCGCGACTAGACTTAGGGGAATTGAAAAGACTTTATACATCTCAGAAGGTGCCTTTGAAGGTCCTGTCCAAC
 TGAGGTATTTGAACCTTGCCATGTGCAACCTTCGGGAATCCCTTAACCTCACACCGCTCATAAAGACTAGATGAG
 CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCTGGCTCTTTCCAGGGTTGATGCACCTTCAAAAAT
 GTGGATGATACAGTCCAGATTCAAGTATTGAACGGAATGCCCTTGACAACCTTCAGTCACTAGTGAGATCA
 ACCTGGCACACAATAATCAACATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACAT
 TTACATCACAAACCTTGAACCTGTAACCTGTGACATCTGTGGCTCAGTGGTGATAAAGACATGGCCCCCTC
 GAACACAGCTTGTGTGCGCGGTGTAACACTCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA
 ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCT
 GAGCTGAAATGTGCGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACA
 TGGGGCGTACAAGTGCAGATAGCTGTGCTCAGTGATGGTCACTTAATTTACAAATGTAAGTGTGAAGTGTGCA
 CAGGCATGTACACATGTATGTTGAGTAATTCGTTGGGAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCA
 GCAACCACTACTCCTTTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
 GACCACAGATAAACAATGTGGGTCCCACCTCCAGTGGTGCAGTGGGAGACCACCAATGTGACCACCTCTCTCACAC
 CACAGAGCACAAAGTGCAGAGAAAACTTCACCATCCCAGTGACTGATATAAACAGTGGGATCCCGGAAT
 GATGAGGTGATGAAGACTACCAAAATCATCATTGGTGTGTTGTGGCCATCACACTCATGGCTGAGTGATGCT
 GGTCAATTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCAACAAGGACTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGGAGACACACCATGGAAAGCCACTGCCATGCTGCTATCAGCATGAG
 CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAGTTAACACAATAAATTCATATACA
 CAGTTCACTGTCATGAACCGTTATTGATCCGAATGAACCTCTAAAGCAATGTACAAGAGACTCAATCT**CA**AAACA
 TTTACAGAGTTACAAAAACAACAATCAAAAAAAGACAGTTTATTAATAAATGACACAATAAGTACTGGGCTAA
 ATCTACTGTTTCAAAAAGTGTCTTTACAAAAAACA AAAAAGAAATTTATTTATTAATAATCTTATTG
 TGATCTAAAGCAGACAAAA

FIGURE 314

MLNKMTLHPQQIMIGRPRFNALFDPLLVLALLQQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
 VRKNLREVPDGI STNTRLNLHENQIQIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
 NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
 YISEGAFEGLSNRLYNLAMCNLREIPNLTPLIKLELDLSGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLVNTEGMAAE
 LKCRASLTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTNLFTNVTVDQTMGYTCMVNSVGN
 TTASATLNVTAATTTFFSYFSTVTVETMEPSQDEARTDNNVGPTPVVDWETTNVTTSLTPQ
 STRSTKFTTIPVTDINSIGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHHQRN
 HHAPTRTVEIINVDDEITGDTPMESHLMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
 VHEPLLRMSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGGGGGCCGGCTCCGCGCCGGCACAT
 GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCGCCAGCTCGCCCGAGGTCGCTCGGA
 GCGCGCCGGCGCCCGGAGCCAGCAGCAACTGAGCGGGGAAGCGCCCGCTCCGGGGATC
 GG**GATG**TCCCTCCTCCTCTCCTCTTGCTAGTTTCTACTATGTTGGAACCTTGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGTCACTTTGCCCTGCCACCATCAACTGGGGC
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCAGATAATGAAGGGGAACCAAAAA
 GTGGTGATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
 AGTGGCCTTTGCTTCCAATTTCTTGGCAGGAGATGCCTCCTTGCGAGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT
 GTCATCTTAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
 AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCACTCCTCTGGCACAGAGCCCATTTGTGTATT
 ACTGGCAGCGAATCCGAGAGAAAAGAGGAGAGGATGAACGCTCTGCCTCCCAATCTAGGATT
 GACTACAACCACCCTGGACGAGTTCTGCTGCAGAACTCTTACCATGTCTACTCTGGACTGTA
 CCAGTGACACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAAGCTACAGT
 ATGTACAAGCATCGGCATGGTTGACAGGAGCAGTACAGGCGATAGTGGCTGAAGCCCTGCTG
 ATTTTCTCCTTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAGAAAGATATGAGGAAGAAGA
 GAGACCTAATGAAATTGAGAAGATGCTGAAGCTCCAAAGCCCGTCTTTGTGAAACCCAGCT
 CCTCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCACTCGCTCCACGCAAAAT
 AGTGCCTCACGCGAGCGGACACTGTCAACTGACGAGCAGCCAGCCAGGGCTGGCCAC
 CCAGGCGATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATG
 CTAATCTGACCAAGCAGAAACCACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA
 ACGGTC**TGA**ATTACAATGGACTTGACTCCCACGCTTTCTTAGGAGTCAGGGTCTTTGGACTC
 TTCTCGTCATTGGAGCTCAAGTCACCAAGCCACACAACAGATGAGAGGTCATCTAAGTAGCA
 GTGAGCATTGACGGAACAGATTGAGATGAGCATTTTCTTATACAAATACCAACAAGCAAA
 AGGATGTAAGCTGATTCTATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG
 AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAGAGTG
 AGGTGAATATACCTAAAACCTTTAATGTGGGATATTTGTATCAGTGCTTTGATTACAATTT
 TTCAAGAGGAAATGGGATGCTGTTTGTAATTTTCTATGCATTTCTGCAACTTATTGGATT
 ATTAGTTATTGAGACAGTCAAGCAGAAACCACAGCCTTATTACACCTGTCTACACCATGTAC
 TGAGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
 TTCAATTTGTCATAAGGTTTGGATATTAAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
 AGAGTGATGAGTTTCTCCACTCTATACATACTCACTATTGTTATTGAGCCCAAAATAAC
 TATGAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT
 ATGAGGATTGTTGACAAACATTAGAAAATATATAATGGAGCAATTTGTGGATTTCCTCCAAAT
 CAGATGCCTCTAAGGACTTCTCTGCTAGATATTCTGGAAGGAGAAAAATACAACATGTCAAT
 TATCAACGCTCTTAGAAAAGAAATCTCTCTAGAGAAAAAGGATCTAGGAATGCTGAAAGATTA
 CCCAACATACCATTATAGTCTCTTCTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG
 GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
 TGGTGCCAGGCACCTGTAGGAAAAATCCAGCAGGTGGAGGTTGCGAGTGAGCCGAGATTATGCC
 ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLMTSYSGLYQCTAGNEAGKESCVVRVTQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFAQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

CGCGAGGCGGCGGGAGCCTGGGACCAGGAGCGAGAGCGCCCTACCTGCAGCGCCGCCACGGCACGGCAGCCCA
 CCTGCGCCCTCTGCTGCTTCGTGCTCCTGTGCGGAGTAGTGGATTTCGCCAGAAAGTTTGGATATCACTACT
 CCTGAAGAGATGATTGAAAAAGCCAAAGGGGAAACTGCCATATCTGCCATGCAAAATTTACGCTTAGTCCCGAAGA
 CACGGGACCGGTGGACATCGAGTGGCTGATATCACCAGCTGATAATCAGAAGTGGATCAAGTGATTATTTTAT
 ATTCTGGAGACAAAATTTATGATGACTACTATCCAGATCTGAAAGCCCGAGTACATTTTACGAGTAATGATCTC
 AAATCTGGTGTGATCATCAATAAATGTAACGAATTTAACTACTCAGATATTGGCACATATCAGTGCAAAAGTGAA
 AAAAGCTCTGGTGTTCCAAATAAGAAGATTCTCTGGTAGTTCTTTGTAAGCCTTCAGGTGGCAGATGTTACG
 TTGATGGATCTGAAGAAATGGGAATGACTTTAAGATAAAATGGAACCAAAGAAAGTTTCACTTCATTACAG
 TATGAGTGGCAAAATTTCTCTACTCACAGAAATGCCACTTCATGGTTAGCAAAATGACTTCATCTGTTAT
 ATCTGTAATAAAATCCCTCTTCTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAACAGAGTGGGCTCTGATC
 AGTGCTCTTCCGCTTAAACGTTGTCCCTCTTCAAATAAGCTGGACTAATTGCAGGAGCCATTATAGGAAT
 TTGCTTCTCTAGCGCTCATTGGTCTTATCATCTTTTGTGTCGTAAAAAGCGCAGAGAAAGAAAATATGAAAA
 GGAAGTTTCATCAGGATATCAGGAAGATGTGCCACCTCCAAAGAGCGGTACGTCCTGCGCAGAAAGCTACATCG
 GCAGTAATCATTCCTCCGGGTCATGTCTCCTTCCAAACATGGAAGGATATTCGAAGACTCAGTATAACCAA
 GTACCAAGTGAAGACTTTGAAGCCTCCTCAGAGTCCGACTCTCCACCTGCTAAGTCAAGTACCTTACAA
 GACTGATGGAATTACAGTTGTAATAATATGGAATCTGAGAATCTGAAGTATTGTATTTTGACTTTATTT
 AGGCCCTCTAGTAAAGACTTAATGTTTTTTAAAAAAGCACAGGCGACAGAGATTAGAGCAGCTGTAAGAACAC
 ATCTACTTTATGCAATGGCATTAGACATGTAAGTCAGATGTCTGTAATATTAGTACGAGCCAAATCTTTGT
 TAAAAAACCTATGTATAGTGACACTGATAGTTAAAGATGTTTTATTATATTTTCAATAACTACCCTAACAA
 ATTTTTAACTTTTCATATGCATATTTCTGATATGTGGTCTTTAGGAAAAGTATGGTTAATAGTTGATTTTCAA
 AGGAAATTTTAAATTTCTACGTCTGTTTAATGTTTTTGTATTTAGTTAAATACATTGAAGGGAATACCCG
 TTCTTTTCCCTTTTATGCACACACAGAAACACGCGTTGTCTGCTCAAACTATTTTATTATGCAACTACA
 TGATTTACACAAATCTCTTAAACACACACATAAAATAGATTTCTTGTATATAAATAACTTACATACGCTTCA
 TAAAGTAAATTTCTAAAGTGCTAGAACAAATCTGCCACTTCTACAGTGTCTCGTATCCAAACAGAGTTGATGC
 ACAATATATAAATCTCAAGTCCAAATATTAATACTTAGGCACTTGACTAATTTAATAAAATTTCTCAAATA
 TATCAATATCTAAAGTGATATATTTTTTAAGAAAGATTATCTCAATACTTTTATGAGTATTAAGTTTATGATGG
 TTTGGCCACTCAACTTCACTACTATTAGTAAGAACTTTTAACTTTTAATGTGTAGTAAAGGTTATCTCACTCT
 TTTCTCAACATGACACCAACACAAATCAAAAACGAAGTTAGTGAGTGTCAACATGTGAGGATTATCCAGTGAT
 TCCGGTCACATGCATCCAGGAGGAGGTACCCATGTCACTGGAATTGGCGATATGGTTTATTTTCTCTCC
 TGATTTGGATAACCAAATGGAACAGGAGGAGGATAGTGATCTGATGGCCATTCCCTCGATACATCTCTGGCTT
 TTTTCTGGGCAAGGGTGCCACATTTGAAGAGGTGGAATATAAGTTCTGAAATCTGTAGGGAAGGAACACAT
 TAAGTTAATTTCAAAGGAAAAAATCATCATCTATGTTCCAGATTTCTCAATTAAGACAAAGTTACCCACAACACT
 GAGATCACATCTAAGTGACACTCTCTATTGTCAAGTCTAAATACATTAATAACCTCATGTCTAATAGGCTATAA
 TGTATACAGGTGACCAATGTTTTCTGAATGCATAAAGAAATGAATAACTCAACACAGTACTCTTCAAAACAA
 CTTCAACCAAAAAGACCAAAACATGGAACGAATGGAAGCTTTGTAAGACATGCTTTGTTTTAGTCCAGTGTTTT
 CCACAGCTTGGCTGAAGCCAGGTGACTTGGAGCTTTTAAATACAAACAAATGGAAGTGGAGGACTTATCTCTT
 AGCAAACTAATGCAGAAACGAAATCACTACCGCATCTTCTCACTTATAAGTGGGAGTATGATAGAACT
 TATGAACCAAAAGAGGAAACATAGACATTGGAGCTTATTTGAGAGGGGAGGTTGGGAGAGGAAAGGAGCA
 GAAAGATAACTATTGACTACTGCTTCAACCTGGGTGATGAATTAATGTGACAAATCTCTGACACAA
 TTTTACCTATGCAACAACTTCTATGTATCCCTAAACCTAAATAAAGTTTAAAAAAGGTTTAAAAAAGGTTTAAAAA
 AAAAAAAGGTTTAAAAAAGGTTTAAAAAAGGTTTAAAAAAGGTTTAAAAAAGGTTTAAAAAAGGTTTAAAAA
 AAAAAAAGGTTTAAAAAAGGTTTAAAAAAGGTTTAAAAAAGGTTTAAAAAAGGTTTAAAAAAGGTTTAAAAA

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVDFARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGGLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARCVDGSEEIGSDFIKCEPKEGSLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTFPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCCTGATTTGGTGA
 ATGGTGAAGGTGCCTGTCTAATTTTTCTGTAAAAAGAACAGCTGCCTCCAGGCAGCCAGCC
 CTCAGGATCAGCTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGACATGAAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC
 CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTGTGTCTCCCTTGCCCTGGGTTTTACCCTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCAGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAAGCTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCTGCTGGAGTTCTACTTGAAAAGCTGTTTTCAAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACT
 TTGTTCTCATCGTGTCACAACTGCAACCCAGTCAAGAAATGAGATGTTTTCCATCAGAGAC
 AGTGCACACAGGCGGTTTCTGTCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
 TCTGACCAAAGCCCTTGGGGAAGTGACATTCTTCTGACCTGGATGCAGAAATTCTACAAGC
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCAATTTCA
 AACAGTCTCCCTTCCTATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTC
 TTGGCCCAGGATTATTGTCAAAGAAGTCATCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCCTCTGGATGCTGTGAAGAGCTACAGAGAAGATTCTTGATTTATTACAACTCTATTT
 AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGAGGATGCTTGGATGTAAACTGAACCTCAGAGCATGAAATCACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGTAAGGTGCATCTGTTTGAAG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAGCAGATCCTCAATAAACATTTTATT
 TCCCACCCACACTGCCAGCTACCCCATCATCCCTTCCCTTGGTGCCCTCCTTTTTTTTT
 TATCCTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAGACACATAA
 CTCCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRQLQSLWTLARPFPCPLLATASQMOMVVLPCLGFTLLLSQVSGAQGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRLFFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC
 CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTT
 CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
 ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAAGCCCTTA
 GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
 TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
 TGCAGAAAACTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
 AATGCCACCAGAGTCATCCATGACAACATATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
 ATCCCTGGGAGAGCTCGACGTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
 CAGCTTGATAGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCCTGTGCGGTTTACT
 GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGACAGCTGAAAGTCC
 CACTGGCTGGCCTCAGGCTGTCTTATTCGGCTTGAAAATAGGCAAAAGTCTACTGTGGTAT
 TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
 CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
 GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATCCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRLISTDMHHIEESFQEIKRAIQAKDTFPNVITLST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
AACGCGGCTACAATTAATACATAACCTTATGTATCATAACATACGATTTAGGTGACACTAT
AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCAGGTCCAAC TGACCTC
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGCCCGCCT
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCTCAGAGCCTATCCCA
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGTGGCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
TGAGCAGAAGATACCTCTGCATGGATTTAGAGGCAACATTTTGGATCACACTATTTTCGAC
CCGGAGAAGTGCAGGTTCCAACACCAGACGCTGGAACACGGGTACGACGTCTACCACTCTCC
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
CACCCCCGTACTCCAGTTCTCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTCAACACC
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
GCTGAAGCCCCGGGCCCGGATGACCCGGCCCCGGCCTCCTGTTACAGAGAGCTCCCGAGCG
CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTGAGTGAAC
ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTTCATCTAGGGTGC
CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNI FGSHYFDPENCRFQHQTLENGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRNEIPLIHFNTPIPRRHTRSAEDDSE
RDPLNLVKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA
KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTCTGTCTGGGAGGTTGGGGTCTCTGG
 GAGCTCTGCGAGCCCCAGCACCCGCGAGAGCAGACTGCGATGACAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGACCCGGGCCACGCCGCTCTGGAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCAAAAAACATCTCCAACTTCATGGTGC
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTACAGCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCCTTGACCCGA
 TGACAGCTCTGAAGAGGCAAAGACACTACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCTGTCTCTAGAGAGCAGTGCCCTCTCCGACGGCCCCCATCCAGTCATC
 ACCCGTCTACGGGCTCAGAGAGCAGCGCCTCTCCGACGGCCCCCATCCAGTCATACCCC
 GTCACGGGCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATACCCCGTCTAT
 GGTCCCGGGATCTGATGTCACTCTCTCGCTGAAGCCCTGGTGACTGTGACAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACACTTCCAGCATCCCTGGGGCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC
 CTGACTCCACTGAAGCAAAACACACATCACTGAGGTACAGCCCTCTGCCGAGACCTGTCC
 ACAGCGGCACACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTG
 AAAGTCTCAGGAGCAGCTCCGCTCCATAGAGGCTGGGTGAGAGTGGGCAAAACAACTTC
 CTTTGTCTGGGAGCTCTGCTTCTCTACAGCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
 CTTAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTCCCCACCAGCAGGACCCCT
 CTTCTTCTGTCTCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
 GAGGCCGACACAGACG**TGAG**TGCAGGTGAAATGGAGGTTTCTCTCTCTGCGGCTGAGTG
 TGGCTTCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACCTCACGCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGGTGTCAGGAGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAGAGGGTGTGCCCCTAGCCTG
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGTGAGAGGTACCCAGAGGTTCCCATG
 AAGGCGAGCATGTCCAAGCCCTAACCCAGATGTGGCAACAGGACCTCGCTCATATCCAC
 CGGAGTGATATGATGGGGAGGGGCTTCACTGTTCCAGAGGTGTCCTGGACTCACCTTGG
 CACATGTTCTGTGTTTTCAGTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCTGCA
 TTAAATTCACTCAGTGTGGCCCAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHALETQTLSEA
 ETSSRASTPAGPIPEAETRGAKRISPARETRSFKTSPNFMVLIATSVETSAASGSPEGAGM
 TTVQTITGSDPEEAIFDITLCTDDSSSEAKTLTMDILTLAHTSTEAKGLSSESSASSDGPHPV
 IPTSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLAEALVTVTNI
 EVINCSITEIETTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALSVEFPSY
 VKVSGAAPVSI EAGSAVGKTSFAGSSASSYSPSEAALKNFPTSETPTMDIATKGFPTSRD
 PLPSVPPTTNSRGTNSTLAKITTSAKTTMKPQQPRPRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP-and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGGATTCGCGGTCCTTCCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAGCAAACCTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACCTAACTGAAATTTAAATGTTCTTCGGGGGAGAAGGGAG
 CTTGACTTACACTTTGGTAATAATTTGCTTCTCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCTATTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTTCTTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCAACTGCTACCTATTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTTCTCTTACATGGCCAATTTTCAACAAGCAGTCACCTCCCC
 TAGCCCATCATCACACAGATTATTTCAAAGCCCAACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTACAAATTTTCTCTGATCAGAGAA
 TAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCAGCTACGGTGCGAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCAGGCCACAGCTGGCCACCACAGCTCCACCTGTAAACCACTGTCACCTTCTC
 AGCTCCCACGACCCTCATTTCTACAGTTTTACACGGGCTCGGGCTACACTCCAAGCAATG
 GCTACAAACAGCAGTTCTGACTACCACCTTTACAGCACCCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCTTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCTCCAGGGCAGTGTCCAGAAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGGTGCTCTTCTCTGGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTCGGAATCACTCCGACAGGAACGTTACTCAAGACTGGAT
 TATTTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCAGAAGCCCAATGCAATGAGTTTCTGCTGACTGTCTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAAAATGCCCTTCTGCTTCTCTTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGGCCAGGCTGGAGTGACAGTACGATCTCGGCTCTCACCGCAACCTCCGTCTC
 CTGGGTTCAAGCGATTCTCTGCTGCTCAGCTCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTGTATTTTAGTAGAGACGGGGTTTACCATTGTTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTGTACCAACCTCTCGCCCTCCCAAAGTGCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTATGTTTGGTTTTTGAGAAGGAATGAAGTG
 GGAACCAATTAGGTAATTTTGGGTAATCTGTCTCTAAATATTAGCTAAAAACAAAGCTCT
 ATGTAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTTCTGGTTCCAGATAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGATATTCCTTTAAACTTATT
 CCAGATGTAGTTCTCTCCAATTAATATTTGAATAAATCTTTTGTACTCAA

FIGURE 328

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVVICFLTRLRLSASQNLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEEKWLLIGSLLFGVLFVLVIGLVLLGRILSES LRKRYSRLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCCACGGTGTCAGACGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTGCGTGTCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCTGAAGGGGACACTGTGT
 CCCTGCACTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCTCTCTCTGCTGCTCTGGCACCATTCTATGCAGAAAGAACGCCAGGAGACAAT
 GAAGGGCAGGGTGTCATCCGTGACAGCGCCAGGAGCTCTCGCTCATTGTGACCCGTGTGA
 ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTCGTCTTCCAGGACCCTGCTGTCTCCCTCCCCTCCCCTCTCCAC
 CTTCACGCTCTGGCTACAAACAGCCTGACAGCCCAAGGCAAAGCTCAGCAAACCCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGCCCCCTCATTTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCTCTACCCAGCGACCTCTCTCTGACGGGAGCTCCCGCCCCCCTATGCAGC
 TGGACTCCACCTCAGCAGAGGACACCACTCCAGCTCTCAGCAGTGGCAGCTCTAAGGCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTCTGGTGTCTGAGCCTTCTGTGAGC
 CGCAGGCTGTATCGCCTTCTGACAGCCACTGTCTCTGTGGAGAAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCGTTGACTCGGGAGGAAAGGAAGCC
 CCTTCCAGGCCCTGAGGGGGAGCTGATCTCGATGCTCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCCAGGCCAGCAGT
 GAAGCAGTATGCTGGCTGGATCAGCACCATTCCCAGAAAGCTTCCACCTCAGCCTCAGAG
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCTCCCCAGGCTCTCTCTTGCATTTGCCA
 GCCTGACCTAGAACGCTTTGTGACCCCTGGAGCCAGGCGGTGGCCTTGTCTTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTTACATCCCTGGGCAGAGTACCAGGCTGTGACCCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGG
 CTCATGCCCACTGTGCGGACCTGCCTTCTCCACTCCAGACCCACCTTGTCTTCCCTCCC
 TGGGCTCTCAGACTTAGTCCCACGGTCTCTCTGATCAGCTGGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT
 GTGAAAAACGTTGATTCTGGCCCCACCAAGACCCACAAAACCATCTCTGGGCTTGGTGAC
 GACTCTGAATTTCTAACAATGCCAGTGAAGTGTGCACTTGAGTTTGAAGGCCAGTGGGCCGT
 ATGAACGCTCACACCCCTTGACCTTAGAGTCTGCATTTGGGCTGTGACGCTTCCACCTGCC
 CAATAGATCTGCTCTGCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCTGTCTAAG
 TCCAGGCCCTGGTCAGGTGAGTGCACATTCAGGATAAGCCAGGACCGGCACAGAAGTGG
 TTGCTTTTNCATTTGGCTTCCCTGCGNCCATGCTTCTGGCTTTGGAAAAATGATGAAGA
 AAACCTTGGCTCTTCTTGTCTGGAAGGGTTACTTGCTCTATGGGTCTGGTGGCTAGAGA
 GAAAGGTAGAAAAACAGATGCGACCTAGGTGTCTAAACACAGAGGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA
 GCACAACTACTATTTTTTCTTTTTCCATTATTATTGTTTTTAAAGACAGAATCTCGTGT
 GCTGCCCAGGCTGGAGTGAGTGGCAGATCTGCAAACTCCGCTCTGGGTCCAAGTATT
 CTTCTGCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGACACCACACCTTGGCTAATT
 TTTGACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGAC
 CTCAAATGAGCCTCTGTCTTCACTCTCCAAATGCGGGGATTACAGGCATGACCCACTGT
 TCTGGCCCTATTCTTTTAAAAAGTGAATTAAGAGTTGTTCAAGTATGCAAACTTGGAAAG
 ATGGAGGAGAAAAAGAAAGAAAGAAAAAATGTACCCCATAGCTCTCACCAGACACTCAT
 TATTTCTGTTTTGTGACTTCTTCCACTCTTTCTTCTTACATAAATTTGCCGGTGTCTT
 TTTACAGAGCAATTTATCTGTATATACAATTTGTATCTGCTTTTCCACCTTATCGTTC
 ATCACTTTATTTCCAGCTTCTCTGTGTTTTACAGACCTTTTATAAATAAAATGTTCATCA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLVLVLLWGCLLLPGYEALEGP EEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSIRDSRQELSLIVTLWNLTLDAGEYWCGVEKRGPD E SLLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQQTQPPGLTSPGLYPAATTAKQGKTGA EAPPLPG
TSQYGHERTSQYTGTSPHPATSPFAGSSRPQMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWSRLTAE EKEAPSQAPEGD
VISMPPLHTSEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128